



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 104187

To: Terra Gibbs
Location: CM1-11E12
Art Unit: 1635
Tuesday, September 23, 2003

Case Serial Number: 09/840704

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

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SEARCH REQUEST FORM

Requestor's
Name: _____

Serial
Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 09-23-03

Searcher: Beverlye 4997

Terminal time: 20

Elapsed time: _____

CPU time: _____

Total time: 23

Number of Searches: _____

Number of Databases: 1

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other CEN

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STIC-Biotech/ChemLib

104187

From: Gibbs, Terra
Sent: Wednesday, September 17, 2003 6:11 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

RECEIVED

SEP 22 2003

Please search SEQ ID NO:1 of USSN 09/840,704.

Please do a search in all commercial databases.

*Terra Cotta Gibbs, Ph.D.
Art Unit 1635
CM1, 12A12
703-306-3221*

*SEARCH DIVISION
CCL*

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: September 22, 2003, 15:24:19 ; Search time 4397 Seconds
(without alignments)
16644.831 Million cell updates/sec

Title: US-09-840-704A-1
Perfect score: 1789
Sequence: 1 gaatttcatctgtcgactgct.....aaaaaaaaaaaaaaaaaa 1789

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 288871 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Maximum DB seq length: 0

Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
listing first 45 summaries

Database : GenEmbl *
1: gb_baa: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
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6: gb_pat: *
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13: gb_un: *
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15: em_ba: *
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17: em_hum: *
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19: em_mu: *
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33: em_htg_mus: *
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35: em_htg_rod: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_ty: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1789	100.0	1789	6	AR094181	AR094181 Sequence
2	1789	100.0	1789	6	AR182654	AR182654 Sequence
3	1789	100.0	1789	6	AR205732	AR205732 Sequence
4	1787.4	99.9	1789	6	AR125502	AR125502 Sequence
5	1787.4	99.9	1789	9	HSU40282	U40282 Homo sapien
6	1771.4	99.0	1786	6	AR220508	AR220508 Sequence
7	1693.4	94.7	1780	6	AF017262	AF017262 Sequence
8	1693.4	94.7	1780	6	AC132877	AC132877 Mus muscu
9	1693.4	94.7	1780	6	AX524966	AX524966 Sequence
10	1652.6	92.4	1731	9	BD114433	BD114433 Human nuc
11	1391.6	77.8	1750	10	MNU09479	U94479 Mus musculus
12	1391.2	77.8	1673	10	BC003737	BC003737 Mus muscu
13	1382.2	77.3	1693	10	AF256520	AF256520 Cavia por
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16	1195.8	66.8	1159	6	AX151689	AX151689 Sequence
17	1195.8	66.8	1359	9	HSA277481	AJ277481 Homo sapi
18	1175	65.7	1359	10	AF339194	AF339194 Rattus no
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23	451.2	25.2	567	6	BD151618	BD151618 Primer fo
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37	310.6	17.4	253559	2	AC133708	AC133708 Rattus no
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40	305	17.3	87197	2	AC014071	AC014071 Drosophil
41	305	17.0	163098	3	AC010055	AC010055 Drosophil
42	305	17.0	182960	3	AC010017	AC010017 Drosophil
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45	194.4	10.9	79733	2	G19940	G19940 human STS A

ALIGNMENTS

RESULT 1 AR094181 LOCUS Sequence 1 from patent US 6001622. DNA linear PAT 08-SEP-2000

DEFINITION Sequence 1 from patent US 6001622. DNA linear PAT 08-SEP-2000

ACCESSION AR094181 VERSION GI:10020926

KEYWORDS Integrin-linked kinase and its use

ORGANISM Unknown. Unclassified.

REFERENCE 1 (bases 1 to 1789)
Dedhar,S. and Hannigan,G.

AUTHORS Title: Integrin-linked kinase and its use

JOURNAL Patent: US 6001622-A 1 14-DEC-1999;

FEATURES Location/Qualifiers

source	1 . 1789 /organism="unknown"	Qy	961 ACACACTGGATGCCGTATGGATCCCTCAATGFACTACATGAGGACCAATTGCGT 1020
BASE COUNT	443 a 489 C 480 G 377 t	Db	961 ACACACTGGATGCCGTATGGATCCCTCAATGFACTACATGAGGACCAATTGCGT 1020
ORIGIN			
Query Match	100 0%; Score 1789; DB 6; Length 1789;	Qy	1021 GTGGACCAGGCCAGGCCTGTGAAGTTGGCATGGCACATGGCCCTCCATA 1080
Best Local Similarity	100.0%; Pred. No. 0;	Db	1021 GTGGACCAGGCCAGGCCTGTGAAGTTGGCATGGCACATGGCCCTCCATA 1080
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Qy	1 GAATTCTCTGTCGACTCTACACCGGAGTCCCCGAGAGGATCTGAGCCAGT 60	Qy	1141 GAGGACATGACTGCCGAATTAGATGGCTGATGTCAGTGTCTCTTCAAATGTCCTGGT 1200
Db	1 GAATTCTCTGTCGACTCTACACCGGAGTCCCCGAGAGGATCTGAGCCAGT 60	Db	1141 GAGGACATGACTGCCGAATTAGATGGCTGATGTCAGTGTCTCTTCAAATGTCCTGGT 1200
Qy	61 CCCGAGGATAAAGCTGGGTTICATCTCCCTTCCTGGATCACTCCACAGTCCTAGGCT 120	Qy	1201 CGCATSTATGACCCCTCCCTGGTAGCCCCGAAGCTCTGCAAGAAAGCCTGAAGACACA 1260
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Qy	121 TCCCCAATCCAGGGGACTCGGGCGGACGCTGCTATGGAGCAGACATTTCACACTCAGTGC 180	Qy	1261 AACAGACGCTACGAGACATGGAAGTTGGAGTTTGCAAGTGTGGAAACTCGGTGACAGG 1320
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Qy	181 CGGGAGGCCAACGGCAGTCGGCTTGCCTGCGCTTGCCTGACAGACCTCAAC 240	Qy	1321 GAGGTAACCCPTTGCCTGACCTCTCCAAATATGGAGATGGAACTGGGATTGGAGGC 1380
Db	181 CGGGAGGCCAACGGCAGTCGGCTTGCCTGCGCTTGCCTGACAGACCTCAAC 240	Db	1321 GAGGTAACCCPTTGCCTGACCTCTCCAAATATGGAGATGGAACTGGGATTGGAGGC 1380
Qy	241 CAGGGGAGGATCATGGCTTCTCCCTGTGACTGGCCTGCCAGAGGGCGCTGTCT 300	Qy	1381 CTTGGCCCTACATCCCACAGGTTATTCCTCTGTGTAACTGAAGTCATGAAGTCCTGC 1440
Db	241 CAGGGGAGGATCATGGCTTCTCCCTGTGACTGGCCTGCCAGAGGGCGCTGTCT 300	Db	1381 CTTGGCCCTACATCCCACAGGTTATTCCTCTGTGTAACTGAAGTCATGAAGTCCTGC 1440
Qy	301 GTGGTTCGAGTGTGATCATGGGGGGGACGGATCAATGTAATGAAACCTGGGGATGAC 360	Qy	1441 ATGAAAGAACCCCCCTCAAAAGCAGCCAAATTGACATGATTGCGCTTATCCITGGAGAAG 1500
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Qy	361 ACCCCCCCTGCACTGGCAAGCACTGGCTATGGACACCCTGATATTGTGAGCTATGCGAG 420	Qy	1501 ATGCGGAGAACAGTAGGACTCTGGCTGAAAGCTCTGGCCCTGAACTCGAGGTGGGACATGGT 1560
Db	361 ACCCCCCCTGCACTGGCAAGCACTGGCTATGGACACCCTGATATTGTGAGCTATGCGAG 420	Db	1501 ATGCGGAGAACAGTAGGACTCTGGCTGAAAGCTCTGGCCCTGAACTCGAGGTGGGACATGGT 1560
Qy	421 1 TACAAGGCGAGCATCATGAGCTGGTGAATGAAACGGGAAATGGCCCTGACTATGCCGT 480	Qy	1561 TGGGGAAATGGACCCPCCAAAAGCAGCAGGCTCTGGCTCCCGCTCCAGTCAT 1620
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Qy	481 1 TTTGGGGCCAGAGCATGAGCTGGCAGAGGACCTGGTGGCAAATGGGCCCTGTGAGCATC 540	Qy	1621 GGTACTACCCCGAGCTGGGGCTCCATCCCCCTACCCCTACACTGTGCGCAAGAGG 1680
Db	481 1 TTTGGGGCCAGAGCATGAGCTGGCAGAGGACCTGGTGGCAAATGGGCCCTGTGAGCATC 540	Db	1621 GGTACTACCCCGAGCTGGGGCTCCATCCCCCTACCCCTACACTGTGCGCAAGAGG 1680
Qy	541 1 TGTAACAGATGGAGAAGATGAGCTCTGGCAAGCAAGCCAGGACCCCTGAGAGCTTC 600	Qy	1681 GGCGGCTCTGAGCTTGTCACTTCGCCACATGGTCTCCCAACATGGGGATGAGCC 1740
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Qy	781 1 AAGGGCCGCTGGCAGGGCAATGACATGGTCTGTAAGGTGGCTGAAAGTTGGACTGGAGT 840	LOCUS	DNA
Db	781 1 AAGGGCCGCTGGCAGGGCAATGACATGGTCTGTAAGGTGGCTGAAAGTTGGACTGGAGT 840	DEFINITION	Sequence 1 from patent US 6338938.
Qy	841 1 ACAAGGAGGAGGGGACTCAATGAGAGTGTGCCGGTCAGGATTTCGATCCA 900	ACCESSION	AR182654
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Db	901 1 AATGTGCTCCAGTGGCTGCTACAGTGGCTCCCTGCTCATCCACTCTC 960	AUTHORS	Dedhar, S. and Hannigan, G.
Qy	901 1 AATGTGCTCCAGTGGCTGCTACAGTGGCTCCCTGCTCATCCACTCTC 960	TITLE	Integrin-linked kinase and its uses
Db	901 1 AATGTGCTCCAGTGGCTGCTACAGTGGCTCCCTGCTCATCCACTCTC 960	JOURNAL	Patent: US 6338938-A 1 15-JAN-2002;
Qy	901 1 AATGTGCTCCAGTGGCTGCTACAGTGGCTCCCTGCTCATCCACTCTC 960	FEATURES	Location/Qualifiers
Db	901 1 AATGTGCTCCAGTGGCTGCTACAGTGGCTCCCTGCTCATCCACTCTC 960	source	1 . 1789

REFERENCE	2 (bases 1 to 1789)	Db	361 ACCCCCTGGATCTGGCAGTCATGGACACCGTGAATTGTACAGAAGCTATTCGAG 420
AUTHORS	Dedhar S. and Hannigan, G.E.	Qy	421 TACAGGCAGACATTAATGGAGATGAAACCGGAAATGTGCCCTGCACATTCCTGT 480
TITLE	Direct Submission	Db	421 TACAGGCAGACATTAATGGAGATGAAACCGGAAATGTGCCCTGCACATTCCTGT 480
JOURNAL	Submitted (07-NOV-1995) Shoukat Dedhar, Cancer Biology Research, Sunnybrook Health Science Centre and University of Toronto, 2075 Bayview Avenue, North York, Ont. M4N 3M5, Canada	Qy	481 TTTCGGCCAAAGATCAAGTGGAGAGGACTGGCCCTTGTCAGCATC 540
REFERENCE	3 (bases 1 to 1789)	Db	481 TTTCGGCCAAAGATCAAGTGGAGAGGACTGGCCCTTGTCAGCATC 540
AUTHORS	Dedhar S. and Hannigan, G.E.	Qy	481 TTTCGGCCAAAGATCAAGTGGAGAGGACTGGCCCTTGTCAGCATC 540
TITLE	Direct Submission	Db	481 TTTCGGCCAAAGATCAAGTGGAGAGGACTGGCCCTTGTCAGCATC 540
JOURNAL	Submitted (21-MAY-1998) Shoukat Dedhar, Cancer Biology Research, Sunnybrook Health Science Centre and University of Toronto, 2075 Bayview Avenue, North York, Ont. M4N 3M5, Canada	Qy	541 TGTACAAGTAGGGAGATGGCCCTGGAAATGGGCCCCCTGGCATCTGC 600
REMARK	Sequence update by submitter	Db	541 TGTACAAGTAGGGAGATGGCCCTGGAAATGGGCCCCCTGGCATCTGC 600
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	/db_xref="taxon: 9606"	Qy	721 GACTCAAACAGCTTAACCTCTGAGAACTCTGGAGAGCTTGGATGG 780
	/chromosome="11"	Db	721 GACTCAAACAGCTTAACCTCTGAGAACTCTGGAGAGCTTGGATGG 780
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	GRSAVEMIJMRGARINVMRQDDTFQKJHAAAGSHHRDIVOKLJOYKADJNAVNEHGNV	Db	1081 CACACACTAGGCCCTCATCCAGACATGCACTAATAGCCGTAATGTTGAT 1140
	PLHACPMQDQVAEIDLVANGALVISCKYGENPVDAKAKPLRELLRRAEKGQNLN	Qy	1141 GAGGACATGACTGCCCTCATCCAGACATGCACTAATAGCCGTAATGTTGAT 1200
	RIPIYRDTFWRGITPRTRPRNGTLNKHSGIDFQKQINFLKGRIGRQGNDIV	Db	1141 GAGGACATGACTGCCCTCATCCAGACATGCACTAATAGCCGTAATGTTGAT 1200
	VKVLRDNTRSRDFQKQINFLKGRIGRQGNDIV	Qy	1201 CGCATGTATGCCCTCATCCAGACATGCACTAATAGCCGTAATGTTGAT 1140
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	ISMDAVKFSIQCPERMAYAWVAPEALQRKPEDINRSADMWSAFLWELVTRREVPS	Qy	1201 CGCATGTATGCCCTCATCCAGACATGCACTAATAGCCGTAATGTTGAT 1140
	ADISNMEIGKVALKQVALKICNNEDPAPRKPFEMIVPILKMQ	Db	1201 CGCATGTATGCCCTCATCCAGACATGCACTAATAGCCGTAATGTTGAT 1140
	DK"	BASE COUNT	443 a 488 c 480 g 378 t
ORIGIN		Query Match	Score 1787.4; DB 9; Length 1789;
	Best Local Similarity 99.9%; Pred. No. 0;	Mismatches	0; Indels 0; Gaps 0;
	Matches 1788; Conservative	Db	Qy 1 GAATTCACTGTGCACTTACCCGGAGCTCCACACTCCAGCTTCAGGCT 60
		Qy 61 CCCGAGGATAAAAGCTGGGTTCATCTCCCTGGATCACTCCAGCTTCAGGCT 120	
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		Qy 121 TCCCCAATCCAGGGACTGGGGCGGGACCTGGCTATGGACATTTCACTAGTC 180	
		Db 121 TCCCCAATCCAGGGACTGGGGCGGGACCTGGCTATGGACATTTCACTAGTC 180	
		Qy 181 CGGGAGGGCAAGCAGTCGGCTTCCTGGCTGGCTGGACACACCGGAGACCTCAAC 240	
		Db 181 CGGGAGGGCAAGCAGTCGGCTTCCTGGCTGGCTGGACACACCGGAGACCTCAAC 240	
		Qy 241 CAGGGGAGGGCAAGCAGTCGGCTTCCTGGCTGGCTGGACACACCGGAGACCTCAAC 300	
		Db 241 CAGGGGAGGGCAAGCAGTCGGCTTCCTGGCTGGCTGGACACACCGGAGACCTCAAC 300	
		Qy 301 GTGGTGAGATGTTGATCATGGGGGGAGGGATGGATGAC 360	
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		Qy 361 ACCCCCCCTGGAGCCAGTCATGGACACCTGTGATATTGTAGAGCTATTGAG 420	
		Db 361 ACCCCCCCTGGAGCCAGTCATGGACACCTGTGATATTGTAGAGCTATTGAG 420	
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RESULT 6

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Db	1501	ATGCCAGGACAAGTAGGACTGGAGGTCTTCCTGACTCCAGAGGTGGACATGTT	1560	Db	421	TACAAGGCAGACATCATGCGATGAACACGGGATGTGCCCTGCACTATGCCGT	480
QY	1561	TGGGGGATGACCTCCAAAGCAGCAGGCTCTGGTCACTCCCTCCATCCCTACAT	1620	QY	481	TTTSGGCCAGATCACTGGCACAGAACGGGATGTGCCCTGCACTATGCCGT	540
Db	1561	TGGGGGATGACCTCCAAAGCAGCAGGCTCTGGTCACTCCCTCCATCCCTACAT	1620	Db	481	TTTSGGCCAGATCACTGGCACAGAACGGGATGTGCCCTGCACTATGCCGT	540
QY	1621	GGTACTACCCGACCTGGGTCATCCCTCCATCCCTACATGGGAGGTCAGG	1680	QY	541	TGTAACAGATGGAGAGATGGCTTGCACTGGCACATGGGTCATGGGAGGTTCTC	600
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REFERENCE	1	(bases 1 to 1786)		QY	721	GACTCAACAGCTTAACTCTGAGGAAGCTAACGAGAATCACTTGAGAGCTGG	780
AUTHORS	Au-Young, J. and Seilhamer, J.J.			Db	721	GACTCAACAGCTTAACTCTGAGGAAGCTAACGAGAATCACTTGAGAGCTGG	780
TITLE	Composition for the detection of signaling pathway gene expression			QY	781	AAGGCCGCTGGCAGGGAAATGAGATGGCTGAAGGTTGGCTCAGACTGGAGT	840
JOURNAL	Patent: US 6500938-A 2001-12-31-DEC-2002;			Db	781	AAGGCCGCTGGCAGGGAAATGAGATGGCTGAAGGTTGGCTCAGACTGGAGT	840
FEATURES	source			QY	841	ACAAGGAGCAGGAACTTCAAGAAAGTGTCCCCTGCAAGATTCTGCAATCC	900
BASE COUNT	443 a 486 c 479 g 378 t			Db	841	ACAAGGAGCAGGAACTTCAAGAAAGTGTCCCCTGCAAGATTCTGCAATCC	900
ORIGIN				QY	901	ATGTCCTCCAGTGTAGGTGCTGCCAGTCACCTCCCTCATCTACTCTC	960
Query Match	99.0%; Score 17114; DB 6; Length 1786;			Db	901	ATGTCCTCCAGTGTAGGTGCTGCCAGTCACCTCCCTCATCTACTCTC	960
Best Local Similarity	99.8%; Pred. No. 0;	Mismatches	0;	QY	961	ACACACTGGATGCCATACTGCACTTCAGCACTCTC	1020
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QY	121 TCCCCAATCGGGGACTCTGGGCGGACTCTGGGCGGACTCTGGGCGGACTCTGG	180	QY	1081	CACACACTAGGCCCTATCCACAGCACTGACTCAATAGCCGTAGTGTAAATGTTGAT	1140	
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QY	241 CAGGGGAGCAGTCATGGCTCCCTGACTGGCTGGAGAGGCCGCTGTGCT	300	QY	1261	ACAGACGCTAGCAGACATGGGGATTTCAGCTGGCTTGTGGACATGGTACACCG	1320	
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QY	301 GTGGTCTGAGATGTGATCATGGGAGGATCAATGATGAACTGGGAGGATGAC	360	QY	1321	GAGGACATCTGGCTGCACTCTCCATGTGGAGATGTGAAGGGCATGGTACAGA	1440	
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QY	361 ACCCCCTGCTGCTGGAGCCAGTCATGGACACCGTGTATGTACAGAACCTATGCA	420	QY	1381	CTTCGCTTACCATCCACAGGTTTCCTCATGTGTGAATGCTCATGAACTCTG	1497	
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Db	1393	GTTATTCCCTCATGTGTAAGCTCATGAGATCTGCATCAAGACCTGCAAAGC	1452		Db	254	CCCCCTTGACTGGGCCCTGCCAGAGGGCGCTGCTGTTGAGATGTTGATCATGC	313
Qy	1463	GACCCAATTTGACATGATGTTGCTATCCTGTGAGAGATGAGAGTAACTGG	1522		Qy	323	GGGGGACCGATCATGTAATGAGACCTGGGGATGACACCCCTGCATCTGCAGCC	382
Db	1453	GACCCAATTTGACATGATGTTGCTATCCTGTGAGAGATGAGAGTAACTGG	1512		Db	314	GGGGGACCGATCATGTAATGAGACCTGGGGATGACACCCCTGCATCTGCAGCC	373
Qy	1523	AGGTCTTGCTGAATCCAGAGGTCGGGACATGGGAAATGCACTCCCAA	1582		Qy	383	GTCATGGACACCGTGTATGACAGAAGCTGAGTCAGTGTGGGATGACACCCCTGCATCTGCAGCC	442
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Qy	1583	GCAGAGGCCCTCTGGTGCCTCCCCGCTCAGTCATGTTACTACCCAGCC	1641		Qy	443	TGAATGACAACGGGATGTTGCCCCGCTCAGTCATGTTACTACCCAGCC	502
Db	1573	GCAGAGGCCCTCTGGTGCCTCCCCGCTCAGTCATGTTACTACCCAGCC	1632		Db	434	TGAATGACAACGGGATGTTGCCCCGCTCAGTCATGTTACTACCCAGCC	493
Qy	1642	GCATCCCTTCCCCATCCTTACACTGTG-CGAAAGGGGGGGCTCAGACSTTGT	1659		Qy	503	CAGAGGCTGGGCAAATGGGGCTTGTGAGATGTTGCTGAGATGAGATG	562
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RESULT 8					Qy	683	GGCCCGGAATGGAACCTGACAAACACTCTGGATTGACTTCAACAGCTTACTCC	742
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DEFINITION		Sequence 13 from Patent EP1236799.			Qy	743	TGACCGAGCTCAACGAGAATCTGTGAGAGTATGGAGGGCGCTGCGAGGCAATG	802
ACCESSION	AX24966				Db	734	TGACCGAGCTCAACGAGAATCTGTGAGAGTATGGAGGGCGCTGCGAGGCAATG	793
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KEYWORDS					Db	794	ACATGGCTGAATGTCAGGAACTCTGGATTGACTTCAACAGCTTACTCC	853
SOURCE	Homo sapiens (human)				Qy	863	ATGAGAGGTCCCCGGCTCAGGATTTCGATCCAAATGTGCTCCAGTGTAGTG	922
ORGANISM	Homo sapiens				Db	854	ATGAGAGGTCCCCGGCTCAGGATTTCGATCCAAATGTGCTCCAGTGTAGTG	913
MATERIAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				Qy	923	CCTGCCAGTCTCACCTGTCAGGTTCTCATCACACACTGGA+GCCATG	982
REFERENCE	1	Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and Rosenthal,A.			Db	914	CCTGCCAGTCTCACCTGTCCTCATCTACTCTCATCACACACTGGA+GCCATG	973
AUTHORS		Human nucleic acid sequences derived from breast tumor tissue pattern: EP 1236799-A 13 04-SEP-2002; metagen Pharmaceuticals GmbH (DE)			Qy	983	CCCTCTACATGACTACTGAGGACCAATTGCTGGGACAGGCCAGCTG	1042
JOURNAL		Location/Qualifiers			Db	974	CCCTCTACATGACTACTGAGGACCAATTGCTGGGACAGGCCAGCTG	1033
FEATURES	source	1.. 1780			Qy	1043	AGTTGCTTGGACATGCGAAGGGCATGCCCTCTCACACACTGAGGCCCTG	1102
BASE COUNT	427 a 489 C 492 g 372 t				Db	1034	AGTTGCTTGGACATGCGAAGGGCATGCCCTCTCACACACTGAGGCCCTG	1093
ORIGIN					Qy	1103	CACGACATGACTCATGAGGCTGAGTCAGTGTGAGGACATGACTGCCGAATTA	1162
Query Match	94 %	Score 1693; DB 6; Length 1780;			Db	1094	CACGACATGACTCATGAGGCTGAGTCAGTGTGAGGACATGACTGCCGAATTA	1153
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Matches 1745; Conservative 0; Mismatches 11; Indels 5; Gaps 4;					Db	1154	GCATGCTGAGTCAGTGTGAGGACATGACTGCCGAATTA	1213
Qy	24	ACGGAGGTCCCAGGAGATCTGCAGCCGAGTCCAGGATAAGCTTGGGTC	83		Qy	1223	TAGCCCCGAGCTGTCAGGAGTCAGGAGACACAGGGCTCAGCAGACATG	1282
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Qy	143	GCCGGAGCAGCTATGACCAATTTCAGTCAGGAGGAGCAACCGAGTGGCG	202		Qy	1343	CCATTGAGATGAGAAGTGGCAATTGGAGGCTTGCCTACATCCACAG	1402
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Qy	203	TTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	262					
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RESULT 9
 BD134433 1780 bp DNA linear PAT 18-SEP-2002
 DEFINITION Human nucleic acid sequence originating in mammary tumor tissue.

REFERENCE BD134433
 VERSION GI:23229378
 KEYWORDS SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Specht,T., Hinzman,B., Armin,S., Pirarski,C., Edgar,D. and Rosenthal,A.

TITLE Human nucleic acid sequence originating in mammary tumor tissue
 JOURNAL METAGEN GESELLSCHAFT FUR GENOME FORSCHUNG MBH
 COMMENT OS Homo sapiens (human)

PD JP 2002516643-A/11
 PD 05-MAR-2002
 PF 19-MAR-1999 JP 20000536852
 PD 20-MAR-1998 DE 198 13 839.3
 THOMAS SPECHT, BERND HINTZMAN, SHCMITT ARMIN, CHRISTIAN PIRARSKI, DUHL EDGAR,
 PI ANDRE ROSENTHAL
 PC C12N15/09, A61K31/711, A61K38/00, A61P35/00, C07K14/47,
 PC C01K16/18,
 PC C12N15/19, C12N5/10, C12N37/02, C12N5/00
 nucleic acid sequence originating in mammary tumor CC
 tissue

KEY Location/Qualifiers
 source 1..1780
 FT /organism='Homo sapiens (human)' .

FEATURES Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 427 a 489 c 492 g 372 t
 ORIGIN

Query Match 94.7%; Score 1693.4; DB 6; Length 1780;

		Best Local Similarity 99.1% ; Pred. No. 0 ; Mismatches 1745 ; Matches 1745 ; Conservative 0 ;
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Db	14	ACGGAGTTCCTGGAGAAGATCTGACGCCGGTCCGAGCTTCAACCTGGGGTTC 73
QY	84	ATCCATCTCCCTGGATCAC-TCCACAGTCCTCAGGCTTCCCACATCCAGGGACTGGG 142
Db	74	ATCCATCTCCCTGGAGCCGAGTCCTCAGCTTCCGAGCTTCCCACATCCAGGGACTGGG 133
QY	143	GCGGGAGCTGCTATGGAGACATTTCACTCACTGCGGGAGGCAAGCGCAAGTGCCTGC 202
Db	134	GCGGGAGCTGCTATGGAGACATTTCACTCACTGCGGGAGGCAAGCGCAAGTGCCTGC 193
QY	203	TTCGCTGTGCTGGATGAAACAGGGGAACCTAACAGGGGGAGCATGCTGCTCTCT 262
Db	194	TTCGCTGTGCTGGACAAACAGGGGAACCTAACAGGGGGAGCATGCTGCTCTCT 253
Db	263	CCCCCTGCAATGGGCTGACTGGCTGCGAGGGGGCTGCGAGGGGGCTGCTGCTGTTAGATGTGATATGC 322
Db	254	CCCCCTGCAATGGGCTGACTGGCTGCGAGGGGGCTGCGAGGGGGCTGCTGCTGTTAGATGTGATATGC 313
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QY	443	TGAATGAAACGGGAAATGGCCCTGGCACTATGGCTGTTTGGGCCAGAATCACTGAGTGG 502
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QY	503	CAGAGGACCTGGCTGCCAAATGGGCCCTGTCAGCATCTGTAACAGATGATGGAGATGC 562
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QY	623	GCCAGAACTCTAACCGTATTCATCAAGGACACATTCTGAAGGGGACCCGACTC 682
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QY	683	GGCCCGAAATGGACACCTGAGCTTCAACAGCTTCAAGGACACATTCTGAAGGGGACCCGACTC 742
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QY	923	CCTGGCAAGTCTCCACACTGGCTCCTACTCTCACACTGGATGCCGTATGG 982
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QY	983	CCCTCTAACATGTAATGAAAGGGACCAATGTCGTTGGACAGAGCCAGGGCTGTGA 1042
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ACCESSION	IMAGE:457801	, complete cds.		
VERSION	BC0011554.1	GI:16306740		
KEYWORDS	MGC,			
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ORGANISM	Homo sapiens			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;				
REFERENCE	1 (bases 1 to 1731)			
AUTHORS	Strasserberg, R.L., Feingold, E.A., Grouse, L.H., Berge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemmer, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Donald, M.R., Cabavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, S., Roqueblano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,			
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Qy 228 GAAAGACCTCAACCAGGGGGAGATCATGGCTTCCCTTGCACTGGGCTCGCGAGA 287	Qy	1308 ACTGGTACACGGGGAGTACCCCTGGCTGACCTCTCCAATATGGAGATGGAAATGGT 1367
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Qy 288 GGGCCGCTCTGCTGCTGGATGGATGGTCAATGGCTATGAA 347	Qy	1368 GGCAATGGAAAGGCCCTTCGGCTTACCATCCCACCAAGGTATTCCCTCAATGGTAAAGCT 1427
Db 200 GGGCCGCTCTGCTGCTGGTGGATGGTCAATGGCTATGAA 259	Db	1280 GGCAATGGAAAGGCCCTTCGGCTTACCATCCCACCAAGGTATTCCCTCAATGGTAAAGCT 1339
Qy 348 CGTGGGGATGACACCCCCCTGCACTGGGCACTCATGGACACGGTAAATGGTACA 407	Qy	1428 CATGAGAGATCTGCAGTAATGGAGACGCCAAATTGACATGATGATGTGCC 1487
Db 260 CGTGGGGATGACACCCCCCTGCACTGGGCACTCATGGACACGGTAAATGGTACA 319	Db	1340 CATGAGAGATCTGCAGTAATGGAGACGCCAAATTGACATGATGATGTGCC 1399
Qy 408 GAAAGCTATGCACTGAGACATCAATGCAATGGTCAATGGCTGCCCCT 467	Qy	1488 TATCCCTGAGAGATTCAGGAAACTAGGACTGGAGGCTCTGGCTGAATCTCGAGAGT 1547
Db 320 GAAAGCTATGCACTGAGACATCAATGCAATGGTCAATGGCTGCCCCT 379	Db	1400 TATCCCTGAGAGATTCAGGAAACTAGGACTGGAGGCTCTGGCTGAATCTCGAGAGT 1459
Qy 468 GCACATGCGCTGTTGGGCCAAGATCAATGGCAGAGGACCTGGCAAAATGGGC 527	Qy	1548 GTCGGGACATGTTGGGGAAATGGCACTTCCCACCAAGGGCCCTCTGGCTTCCC 1607
Db 380 GCACATGCGCTGTTGGGCCAAGATCAATGGCAGAGGACCTGGCAAAATGGGC 439	Db	1460 GTCGGGACATGTTGGGGAAATGGCACTTCCCACCAAGGGCCCTCTGGCTTCCC 1519
Qy 528 CCTGGTCA GCATCTGTAACAGTATGGAGATGCTGTGAGCAAAGCAGGCAACCT 587	Qy	1608 CGCCCTCAGCATGGTACTAACCCCGGCC - TGGGGTCCATCCCTTCCCCTACCA 1666
Db 440 CCTTGTCAGCATCTGTAACAGTATGGAGATGCTGTGAGCAAAGCAGGCAACCT 499	Db	1520 CGCCCTCAGCATGGTACTAACCCCGGCCATGGGTCATCCCTTCCCCTACCA 1579
Qy 588 GAGAGACCTCTCCGAGAGGGCCAGAGAAGATGGCCAGATCTCAACCGTATCCATA 647	Qy	1667 CTGTG - CGCAAGGGGGGGCTAGAGTGGTCAATGGTCACTTGGCTCCAAAC 1724
Db 500 GAGAGACCATCTGGAGGGGAGCACCCGGACTCGGCCAGATCAATGGGCAACTCGGCC 619	Db	1580 CTGTGCCCCAAGGGGGGGCTAGAGTGGTCACTTGGCTCCAAAC 1639
Qy 708 AACACTGGCATTTGACTTAAACAGCTTAACCTCTGAGCTCAAGGAAATCACTC 767	Qy	1725 ATGGGAGGGATCAGCCCCGGCTGTACAATAAAGTTATTATGAAAAAAA 1784
Db 620 AACACTGGCATTTGACTTAAACAGCTTAACCTCTGAGCTCAAGGAAATCACTC 679	Db	1640 ATGGGAGGGATCAGCCCCGGCTGTACAATAAAGTTATTATGAAAAAAA 1699
Qy 768 TGGAGAGCTATGAAAGGGCCGGCAATGACATTTGCTGTAAGGGTCTGAAGGT 827	Qy	1785 AAAA 1789
Db 680 TGGAGACCTATGAAAGGGCCGGCAATGACATTTGCTGTAAGGGTCTGAAGGT 739	Db	1700 AAAA 1704
RESULT 1.1 MMU94479 1750 bp mRNA linear DEFINITION Mus musculus integrin binding protein kinase mRNA, complete cds.		
LOCUS U94479	MUS	Mus musculus
ACCESSION U94479	integрин	Integrin
VERSION 1	binding	binding
KEYWORDS	protein	protein
SOURCE	mouse	mouse
ORGANISM	Mus musculus	Mus musculus
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1	Li, F., Liu, J., Mayne, R. and Wu, C.	Li, F., Liu, J., Mayne, R. and Wu, C.
AUTHORS	Identification and characterization of a mouse protein kinase that	Identification and characterization of a mouse protein kinase that
TITLE	is highly homologous to human integrin-linked kinase	is highly homologous to human integrin-linked kinase
JOURNAL	Biochem. Biophys. Acta 1358 (3), 215-220 (1997)	Biochem. Biophys. Acta 1358 (3), 215-220 (1997)
MEDLINE 98031580		
PUBMED 9366252		
REFERENCE 2	(bases 1 to 1750)	(bases 1 to 1750)
AUTHORS	Wu, C. and Li, F.	Wu, C. and Li, F.
TITLE Direct Submission		
JOURNAL Birmingham, 1670 University Blvd., 217 Volker Hall, Birmingham, AL 35294-0019, USA		
FEATURES Location/Qualifiers	Source	Source
	1..1750	1..1750

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	PHYACFGQDODVAEDVANGALKAPELLELLRERVQHGRQGNDIV	
	RFPKDITWKGTRTRPRNGTFLNKHSGLDFKQJNPLAKUNENSGELWGRKGNDIV	
	VKULKVRWMSTRXKRDNEBECPRTRFSPNPUVFLVGLACQAPPAHPHTLTHWPGS	
	LYNLHECTNFNUVOSQAVKEPLMARGAEFLHITPRHALNSWV	
	ISMDVKVFSQCPERMVAPAWVAEALQKPEDINRRADMMNSFAVILWELVTEEVPF	
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	DK"	
BASE COUNT	436 a 464 c 463 g 387 t	
ORIGIN		
Query Match	77.8%; Score 1391; DB 10; Length 1750;	
Best Local Similarity	90.0%; Bred. No. 0;	
Matches	1514; Conservative 0; Mismatches 164; Indels 4; Gaps 2;	
Qy		
112 CCTCTAGGCTTCGCCATCCAGGGACTCGGGCGGAGCCTGCTATGGACAGCATTTTC	171	
69 CCCGAGGCTTCGCCAGTCCGGGTCTCTGCGCCGGAGCGACATTTC	128	
Db		
172 ACTCTAGTGCGGGAGCGCAAGCACTCGGCCCTCCTGCGCTGACACACGGAGAC	231	
129 ACTCTAGTGCGGGAGCGCAAGCGGGTGGCGCTTGCGACAACACAGAAC	188	
Qy		
232 GACCTCAACCGGGGACGATCTATGCCTTCTCCCTTGACTGGGCTCGGGAGGGC	291	
189 GACCTCAATCGGGGATGATCATGCTCTCCCTTGACTGGCTCTCGAGAGC	248	
Db		
292 CGCTCTGCTGTGGTGGAGATGTGATCATCGGGGGCACGATCAATGATACTGACCT	351	
249 GCCTCTGGGGTGTAACTGATCATGCTGGAGACAGCGATTAATGCTGATGATCTG	308	
Qy		
352 GGGGGTACACCCCTGCACTGCACTGCAACCCGTTGATATGTCAGAC	411	
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412 CTATCCAGTCAAGGAGCACTAATGCACTGCAATGCAACCGGAATGTGCCCTGCA	471	
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Db		
472 TATGCCGTGTTTGGGCCAAGATCAAGTCACTGCACTGCAATGGGCCCTT	531	
429 TATGCACTGTTCTGGGCCAAGACGACGGTGGCTCTGCACTGCACTGCACTG	488	
Qy		
532 GTCACCATCTGTAACAGTATGGAGAGATCTGCACTGCAACGGCAAGCCCTGAGA	591	
489 GTGASCATCTGTAACAGTATGGAGAGATCTGCACTGCAACGGCAACCCCTTGA	548	
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592 GAGCTCTCCGAGGGGACACTCGCACAGAACGCAAGCCGAACTGCACTGCA	651	
549 GAGCTCTCCGAGAACGGGGAGAAATGCGCAGATCPCAACGGTATCCATACAG	608	
Db		
652 GACACATCTGAGGGGACACCCACACTGGCCCGAATGGACCCCTGACAAACAC	711	
609 GACACATCTGAGGGGACACTCGCACAGAACGCAAGCCGAACTGCACTGCA	668	
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Qy		
772 GAGCTATGGAGGGCCCTGGCAGGGCAATCACATGTCGTAAGGTCTCAAGGTGCA	831	
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Qy	832 GACTGGGTAACAGGAGACGGACTCTCAATGAGGAGTGTCCCCGGCTCAGGATTC	891
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Qy	892 TCGCATCAAATGTCCTCCAGTGCTGTTGCTGCTCCACTCTCCACCTCTCATCT	951
Db	849 TCACACCTAACGCTCTCCAGTGCTGCTGCTCCAGCTCCCCACCCA	908
Qy	952 ACTCTACACACTGGTGCCTATGATCTCTCAATGACTCATGAGGAC 1011	
Db	909 ACCCTCATCACACACTGGTGCCTATGATCTCTACATGATGTCATGAAGGAC	968
Qy	1012 ATTTGCTGTCGACAGGACGCCAGGGCTGAGTTGCTTGTGACATGGCAAGGGCATG	1071
Db	969 AATTCTGCTGACAGGACGCCAGCTGATGACATGGCAAGGGCATG	1028
Qy	1072 GCCTCTACACACTAGAGCCCTCTCCAGACATGACTCAATGAGGACACC	1131
Db	1029 GCTTCTCACACACTAGACGCTCTCACACCCGGATGACTCAATGCCGAGTGA	1088
Qy	1132 ATGATGATGAGGAGATGACTGCCGATATTAGATGGATGTCAGTCAGTCTTCTCAA	1191
Db	1089 ATGATGATGAGGATGATGACTGCCGATCAGATGCTGATGTTAAGTTTCTCTCAG	1148
Qy	1192 TGCTCTGTCGCTATGATGACCTGCTGCTGGTAGCCCGAAGTCGCTGAGAAGGCT	1251
Db	1149 TGCCCTGGGCCTATGCGCTCCCTGGCTGCTGCGCCCTGAGCCTGAGAAGGAC	1208
Qy	1252 GAAGACAAACAGAGCTCAGCAGACATGCTGAGCTGAGCTGAGAAGGCT	1311
Db	1209 GAAGACAAACAGAGCTGAGCAGACATGCTGAGAAGGACTGAGGACTG	1268
Qy	1312 GTGACAGGAGGACTTGTGACTGCTCCATATGAGATGGAATGAGSTGGCA	1371
Db	1269 GTGACAGGAGGACTTGTGACTCTCTATATGAGATGGAATGAGSTGGCA	1328
Qy	1372 TTGGANGGCCTTCGACCTACATCCACCGATTTCCTCTCATGTTGTAAGCTATG	1431
Db	1329 CTGGAGGGCCTTCGCCCCTACGTGTCACAGGATTTCCCCCATGTTGTAAGCT	1388
Qy	1432 AAGATCTGCAATGAGACCCCTGCAAGGACCAAAATTGACATGATGTTGCTATC	1491
Db	1389 AAGATTTGATGATGAGACCCCTGCAAGGACCAAGTGTGACATGATGTTGCTATC	1448
Qy	1492 CTTGAAGATGCAAGGAGACTGCACTGCAAGTCACTGCACTGCACTG	1551
Db	1449 TTGGAGAGATGCACTGCAAGGACCAAAATTGACATGATGTTGCTATC	1508
Qy	1552 GGACTGTGGGGAAATGCACTGCAAGGACCCCTGCTGGTGTGCTCCCCGGC	1611
Db	1509 AACATGCTGGGGAGACTCTCAAGTAAAGACTCTGCTGCTGCTCCCTGTC	1568
Qy	1612 TCCAGTGTGACTACCCAG_CCTGGGTCATCCCTTCCCTACCTACTGTC	1670
Db	1569 TCTAATCTGTTACTACCCAGTATGGACTCTGCTCTGCTCCATCTTACACTGT	1628
Qy	1671 --GGCAAGGAGGCGGCTGCACTGTTGACTTGCACATGTTGCTCCACATG	1727
Db	1629 AGCCCAAAAGGGCTGGCTCAGACTTGTACTTGCACATGATGTCCTCCACATG	1688
Qy	1728 GGAGGATCAGGCCGCTGTCACATGAACTGAAAGTATTGAAAGAAAAAAA	1787
Db	1689 GGAGGATCAGGCCGCTGTCACATGAACTGAAAGTATTGAAAGAAAAAAA	1748
Qy	1788 AA 1789	
Db	1749 AA 1750	

BC003737	LOCUS	BC003737	1673	bP	mRNA	linear	ROD 16-APR-2003
DEFINITION	Mus musculus integrin linked kinase, mRNA (cDNA clone MGC:3823 IMAGE:3010214), complete cds.						
VERSION	BC003737	GI:13277656					
KEYWORDS	MGC.						
ORGANISM	Mus musculus (house mouse)						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 1673)						
AUTHORS	Straussberg,R.L., Beingold,E.A., Grouse,L.H., Derge,J.G., Schuler,G.D., Klausner,R.D., Collins,F.S., Wagner,L., Shearer,C.M., Schaefer,C.F., Bhat,N.K., Altschuler,S.F., Zeeberg,B.R., Buetow,K.H., Max,S.I., Wang,J.J., Hsieh,F., Hopkins,R.F., Jordan,H., Moore,T., Farmer,A., Rubin,G.M., Hong,L., Diatchenko,L., Matsunaga,K., Loqueland,J., Peters,G.J., Stepleton,M., Soares,M.B., Ronaldi,M.P., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loqueland,J., Peters,G.J., Abramson,R.D., Mullhy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villaflor,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fayen,J., Helton,E., Kerttman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smilus,D.E., Schnierch,A., Schein,J.E., Jones,S.J. and Marra,M.A.						
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences						
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)						
MEDLINE	22388257						
PUBMED	12477932						
REFERENCE	(bases 1 to 1673)						
AUTHORS	Straussberg,R.						
TITLE	Direct Submission						
JOURNAL	Submitted (28-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA						
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov						
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arranged by: The I.M.A.G.E. Consortium (L1NL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 941305 Web site: http://www.sugc.stanford.edu Contact: (Dickson, Mark) mcc@paxphil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.						
FEATURES	Location/Qualifiers source source						
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	/organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090" /clone="MGC:5823 IMAGE:3601214" /tissue="Mammmary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_id="NCI CGAP_Mam1" /lab_host="DH10B" /note="Vector: pCMV-SPORT6"						

	ORGANISM	Cavia porcellus
QY	842 CAAAGAAGCAGGGACTCTAATGAGAGTGTCCCGGGCTCAGGATTTCCTGCATCAA	901
Db	721 CAAGGAAGAGGAGGGACTCTAATGAGAGTGTCCCGGGCTCAGGATTTCCTGCATCAA	780
QY	902 ATGTGCTCCCACTGCTAGTCTGCGATGTTCTGCCATGAGAATTCCTCCGGCTAGGA	961
Db	781 AGTGTCTCCCACTGCTAGTCTGCGATGTTCTGCCATGAGAATTCCTCCGGCTAGGA	840
QY	962 CACACTGATCGCTTGATGATCCATGACATGACTCTCTCATACAAATGTTCTCATCA	1021
Db	841 CACACTGATCGCTTGATGATCCATGACATGACTCTCTCATACAAATGTTCTCATCA	900
QY	1022 TGGACCCAGGAGCAGGCTGTGAGTTGCTTGGACATGGCAGGGCATGCCCTCTAC	1081
Db	901 TGGACCCAGGAGCAGGCTGTGAGTTGCTTGGACATGGCAGGGCATGCCCTCTAC	960
QY	1082 ACACACTGAGACCCCTCATCCACGACATGACTCATAGCGTAGTGTAAATGATGATG	1141
Db	961 ACACACTGAGACCCCTCATACCCGGATGACTCATAGCGCAGSTGTAAATGATGATG	1020
QY	1142 AGGACATGACTGCCCATGGCTGAGCTGCTGTCAGTCTTCCAGTGGCTCGTC	1201
Db	1021 AGAGATAGACTGCCGATGACATGACTCATGGCTCGTCAGTGGCTCGTC	1080
QY	1202 GCATGATGACCTGCTGGTAGCCCCGAAAGCTCTGCAGAAGAAGCCTGAGAACAA	1261
Db	1081 GCATGATGACCTGCTGGTAGCCCCGAAAGCTCTGCAGAAGAAGCCTGAGAACAA	1140
QY	1262 ACAGAGCCTCACGAGACATGAGCTGTGGAGTTGCTGGACTCTGGAGACTGGACAGG	1321
Db	1141 ACAGAGCCTCACGAGACATGAGCTGTGGAGTTGCTGGAGCTGGACAGG	1200
QY	1322 AGGTACCTTGTGACTCTCCAATATGGAGATGGGATAGGGCATGGAGGC	1381
Db	1201 AGGTGCCCCTGTGACTCTCTAATATGGAGATGGGATAGGGCATGGAGGC	1260
QY	1382 TTGGCCTACCATCCCACCGTATTCCCTCATGTCAGTCAGTCAGATCTGCA	1441
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QY	1442 TGAATGAGACCCCTGCAAGGGACCCAAATTGACATGATGTCGCTATCTTGAGA	1501
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QY	1502 TGCAGGACAAGCTGGAGGTCTGCTGAATCCCGAGGPTCGSACATGGT	1561
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QY	1622 GTACTACCCAG-CCTGGGTCATCCCTTCCCACCTACACTGT--GGCAAG	1677
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QY	1738 GCCCCGCTGACAAATAAGTTTATGAAAAAAA 1789	
Db	1621 GCCCCGCTGACAAATAAGTTTATGAAAAAAA 1672	
RESULT 13		
AF25520		
DEFINITION	AF256520 mRNA linear ROD 13-NOV-2001	
ACCESSION	Cavia porcellus beta-integrin-linked kinase mRNA, complete cds.	
VERSION	AF256520.1 GI:7862154	
SOURCE	Cavia porcellus (domestic guinea pig)	
BASE COUNT	431 a 436 c 449 g 377 t	
ORIGIN		
Query Match	77.3%	Score 1382.2;
Best Local Similarity	90.6%	DB 10; length 1693;
Matches	1531;	Pred. No. 0; Mismatches 148; Indels 10; Gaps 5;
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QY	108 CAGTCTCTGAGCTCCCAATCCAGGGACTCTGGGCC-GGGACGCTGTATGGAGACA	166
Db	66 TTTCACCCAGTGGGGAGGGCACCTGCTGAGTGGCTGAGCTGGCTGAGAACACCG	125
QY	167 TTTCACCCAGTGGGGAGGGCACCTGCTGAGTGGCTGAGCTGGCTGAGAACACCG	226
Db	66 TTTCACCCAGTGGGGAGGGCACCTGCTGAGTGGCTGAGCTGGCTGAGAACACCG	125
QY	227 AGAACGCTCACCGGGGGACATCTGGCTCTCCCTCTGACTGGCCCTGGAG	286
Db	126 AGAACGCTCACCGGGGGACATCTGGCTCTCCCTCTGACTGGCCCTGGAG	185
QY	287 AGGGCGCTCTGCTGGTGAATGTCATGCCGGGGCACGGTCAATGTAATGA	346
Db	186 AGGGCGCTCTGCTGGTGAATGTCATGCCGGGGCACGGTCAATGTAATGA	245
QY	347 ACCGGGGGTGACACCCCTGCTGAGCTGCTGGAGGACATGGAGTATGTAC	406
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QY	407 AGAACGCTCACCGGGGGACATCTGGCTCTCCCTCTGACTGGCCCTGGAG	466
Db	306 AGAACGCTCACCGGGGGACATCTGGCTCTCCCTCTGACTGGCCCTGGAG	365
QY	467 TGCACCTATGCTGTTTGGGCCAGATCAAGTGGAGGACCTGGCGCAATGGG	526
Db	366 TGCACCTATGCTGTTTGGGCCAGACCAAGTGGAGGACCTGGCGCAATGGG	425
QY	527 CCCTGTCAGCATCTGTAACAGTATGGAGAGATGGCGCTGGAGAACGCC	586

Db	426	CCCTCGTCAAGGATTGTATAATAGTAGATGGAGAGATGCCATATGGACAAGCCAAGGACCCC	485	Qy	1664	CCACTGTG---CGCAAGAGGGGGCTCAGAGTTTGTCACCTCCACATGGTGTCTCC	1720
Qy	587	TGAGAGACCTCTCCGAGAGCCGCAGAGAAGATGGCCAGAACTCAACGGTATTCCAT	646	Db	1563	CCACTGTGACCCGAAGGCCCTGGCTAACAGGTGACTCCACAGGTCTCC	1622
Db	486	TGAGAGACCTCTCCGAGAACGAGAGATGGCCAAATCTTAACCGTATTCCAT	545	Qy	1721	CAACATGGGGGGATOAAGCCGCTGTCAAATAAAGTTTATTAGAAAAAAA	1780
Db	647	ACAAGGACACATTCCTGAAGGGACCACCCGACTGGCCGAATGGACACCCTGAA	706	Db	1623	CAGCATGGGGATCAGCCCTGCCTGACATGAA	1682
Db	546	ACAAGGATACATCTSGAAGGGACCAACGCCACAGGGCCAGAAATGGACCCCTGAA	605	Qy	1781	AAAAAAA	1789
Qy	707	AACACTCTGGATTGACTCTAACAGCTTAACCTCTGACAAGGATCTACT	766	Db	1683	AAAAAAA	1691
Db	606	AACACTCTGGATTGACTCTAACAGCTCAAGCTCAACTTGGCAAGGTCAGAGATCTACT	665	Qy	RESULT	14	
Qy	767	CTGGAGAGCTATGGAGGGCGCTGGCAAGGGCAATTGACTCTACATGGTGTGAAAG	826	AC132877	AC132877	192539 bp	DNA linear
Db	666	CTGGAGAGCTATGGAGGGCGCTGGCAAGGGCAATTGACTCTACATGGTGTGAAAG	725	LOCUS	AC132877	192539 bp	HTG 12-MAR-2003
Qy	827	TTCGAGACTGGAGTACAGGAGAGGAGGACTCTAACATGGAGCTCCGGCTCAGGA	886	DEFINITION	Mus musculus clone RP24-216J21,	WORKING DRAFT SEQUENCE,	7 unordered pieces.
Db	726	TTCGAGATTGGAGTACAGGAGAGGAGGACTCTAACATGGAGCTGCCGGCTCAGGA	785	VERSION	AC132877	3	GI:28927732
Qy	887	TTTTCCTGCATCCTAACAGCTGCTAGGCTCTGCACTGCTCCACCTGCTCC	946	KEYWORDS	HTG; HTGS PHASE1; HTGS_DRAFT.		
Db	786	TTTTCCTGCATCCATTGCTCATCACATGGTGTCCAGTGGCTTGGAGATCTGCTCC	845	SOURCE	Mus musculus		
Qy	947	ATCCCTACTCTCATCACACACTGGATGCCPATGGATCCCTACATGTACTCATGAAG	1006	ORGANISM	Eukaryot;		
Db	846	ACCCCTACCTCTATCACACTGGATGCCATGGCTCATCACATGTACTCATGAAG	905	REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteostomi;		
Qy	1007	GCACCAATTGCTCGCGGACAGAGCAGGCTGTGAAGTTGCTTGGACATGGAAAGGG	1066	AUTHORS	Mus musculus; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
Db	906	GCACCAATTGCTCGCGGACAGAGCAGGCTGTGAAGTTGCTTGGACATGGAAAGAG	965	TITLE	Birren,B., Nusbaum,C., and Lander,E.		
Qy	1067	GCATGGCCCTCTTACACAACATAGCTCATCCCCATGACTAAATAGCCGA	1126	JOURNAL	Unpublished		
Db	966	GGATGGGTTCTCTTACATACATAGGCCCTCATCCCCATGACTAAACGCCGA	1025	REFERENCE	1 (bases 1 to 192539)		
Qy	1127	GTGTAATGATGATGAGGACATGACTGCCGAATTAGCATGCCATGGCTGAAAGTTCT	1186	AUTHORS	2 (bases 1 to 192539)		
Db	1026	GTGTAATGATGATGAGGACATGACTGCCGAATTAGCATGCCATGGCTGAAAGTTCT	1085	REFERENCE	Birren,B., Bastien,V., Bloom,T., Bochkovskiy,L., Boukhgalter,B.,		
Qy	1187	TCCAATGTTCTGCTCCATGATGACCTCTGCTGAGCTCTGCGAGAAAGA	1246	AUTHORS	Camarata,J., Chang,J., Chazaro,B., Choepe,Y., Collymore,A.,		
Db	1086	TCCAGTGTCCCTGGCCGATGATGACCTCTGCTGAGCTCTGCGAGAAAGA	1145	REFERENCE	Cook,A., Cooke,P., Dewart,K., Diaz,J.S., Dodge,S.,		
Qy	1247	AGCCTGAAGACAAACGAGGCTCGAGCATGCTGCCATTGCTGAAATGAAAGG	1306	AUTHORS	Faro,S., Ferreira,P., Fitzgerald,M., Dewar,K., Diaz,J.S., Dodge,S.,		
Db	1146	AACCTGAAGACAAACGAGCTCGAGCATGCTGCCATTGCTGAAATGAAAGG	1205	REFERENCE	Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,		
Qy	1307	AACTGGTGGACAGGGGGTACCCCTCTGCTGACCTCTCCAAATATGGAGATGAA	1366	AUTHORS	Horton,L., Huime,W., Iliev,I., Jones,C., Kamat,A.,		
Db	1206	AATTGGTAAACAGGAGGGTACCTTGTGCTGACCTCTCAGTGGATGAAAGG	1265	REFERENCE	Karatas,A., Keills,C., Landers,T., Levine,R., Lindblad-Toh,K.,		
Qy	1367	TGGCATTTGGAGGGCTTCGGCTACCATCCACAGGTTCTCCATGCTTAAGC	1426	AUTHORS	Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,		
Db	1266	TGGCATTTGGAGG--ACGGCTTACATCCACAGGTTCTCCATGCTTAAGC	1322	REFERENCE	McCarthy,M., Melorim,J., Menuez,L., Mihova,T., Mienga,V., Murphy,T., Nguyen,C., Nicoll,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfay,S., Theodorou,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A., and Zody,M.		
Qy	1427	TCTGAGGATGCTGATGATGAGGCTCAAGGACCCAAATTGAGATGATGTC	1486	TITLE	Direct Submission		
Db	1383	CTATCCCTGAGGAGATGAGGCTCAAGGACCCAAATTGAGATGTC	1442	JOURNAL	Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
Qy	1323	TCATGAGATTGCTGATGATGAGGCTCAAGGACCCAAAGCTGTTGAGTGTG	1382	REFERENCE	1 (bases 1 to 192539)		
Db	1487	CTATCCCTGAGGAGATGAGGCTCAAGGACCCAAATTGAGATGTC	1545	AUTHORS	Birren,B., Nusbaum,C., and Lander,E.		
Qy	1428	TCTGAGGAGATGCTGATGAGGCTCAAGGACCCAAATTGAGATGTC	1442	REFERENCE	Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Collymore,A., Cook,A., Cooke,P., Dooley,K., Erickson,J., Faro,S.,		
Db	1383	CTATCCCTGAGGAGATGAGGCTCAAGGACCCAAATTGAGATGTC	1502	AUTHORS	Fitzgerald,M., Hafetz,N., Haigppian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kelis,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Mabitt,R., MacLean,C., McDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Melorim,J., Menuez,L., Mihova,T., Mienga,V., Murphy,T., Nguyen,C., Nicoll,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfay,S., Theodorou,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A., and Zody,M.		
Qy	1606	CCGCCTCTCAGTCATGGTACTACCCAGGCC-TGGGGTCCATCCCTCCATCC	1663	REFERENCE	Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubb,S.M., Talamas,J., Tesfay,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Vie,R., Vo,J., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A., and Zody,M.		
Db	1503	CCTGCCCTCAGTCATGGTACTACCCAGGCC-TGGGGTCCATCCCTCCATCC	1562	AUTHORS			

Qy	11122	CCGTAGTGTGATTGATGATGAGGACATGACTGCCGAATTAGCATGGCTGATGTCAGTT	1181
Db	101343	CTACAGTGTGATTGATGATGAGATATGACTGCCGAATTAGCATGGCTGATGTCAGTT	101402
Qy	11182	CTCTTTCAAATGTCCTGGCGGGTGTATGAGCTGGCTGGTAGCCCCGAAAGCTCTGCA	1241
Db	101403	TCTTTCAGTGCCCTGGCGGGTGTATGAGCTGGCTGGTAGCCCCGAAAGCTCTGCA	101462
Qy	12422	GAAGAAGCCTGAAAGACACAAACAGAGCCTCAGCAGACATGCTGAGCTTGCAGTTCT	1301
Db	101523	GTGGGAACTGGTGAACGGGGTACCCCTTGCTGACCTCTCAATATGGCATTGGAT	101582
Qy	13662	GAAGGGTGCATTGGAAAGCCCTTGCGGCTACCATCCCACACAGTATTCCCTCATGTTG	1421
Db	101583	GAAGGGGCACTGGAGGGCTTGCGGCTACCATCCCACACAGTATTCCCTCATGTTG	101642
Qy	14222	TAAGCTCATGAAAGATCTGATGAATGAAAGAACCCAAATTGGACATGAT	1481
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Qy	14822	TGTGCTTATCCTTGAGAAGATGCGGACAACTAGGACTGGAGGTCTGCTGAATCC	1541
Db	101703	TGTGCTTATCCTTGAGAAGATGCGGACAACTAGGACTGGAGGTCTGCTGAATCC	101762
Qy	15422	AGAGGTGTCGGACATGGTTGGGGAAATGACCTCTCCAAAGCAGGCGCTCTGGTGC	1601
Db	101763	AGAAGTGTAAAACATGGTGGGGAAATGACCTCTCCAAAGCAGGCGCTCTGGTGC	101822
Qy	.16022	CTCCCCCGCTTCAGCTCATGGTACTACCCAGCCAGCTGGGTCTGCTGCATCC	1660
Db	101823	CTCCCCGTCTCTCAATCATGGTATTACCCAGCTGGGTCTGCTGCATCC	101882
Qy	16612	CTTACCACTGT--GCCAAGGGGGCGCTAGAGTTTGTCACTGCCACATGGTGTGTC	1717
Db	101883	CTTACCACTGTAGCCCCAAAGGGCTGGCTCAGGCTTGTCACTGCCACATGGTGTGTC	101942
Qy	17182	TCCCCAACATGGAGGGATCAGCCCCCTGTICAATAAAGTTTATTGAAAAAAA	1777
Db	101943	TCCCCAACATGGAGGGATCAGCCCCCTGTICAATAAAGTTTATTGAAAAAAA	102002
Qy	17782	AAAAAA 1782	
Db	102003	GAAGA 102007	
RESULT 15			
AC093480			
LOCUS	AC093480	209228 bp	DNA linear
DEFINITION	Mus musculus clone RP23-61L24,	WORKING DRAFT SEQUENCE, -4	unordered pieces.
ACCESSION	AC093480	GI:22125292	
VERSION	AC093480.2	HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.	
KEYWORDS		Mus musculus (house mouse)	
SOURCE		Mus musculus	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.	
REFERENCE		1 (bases 1 to 205228)	
AUTHORS	Birren,B., Nusbaum,C. and Lander,E.		
TITLE			
JOURNAL			
REFERENCE	2 (bases 1 to 205228)		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A., Canarino,J., Campopiano,A., Chang,J.J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Devar,K., Diaz,J.S., Dodge,S., Faro,S., Pereira,P., Pitzhugh,W., Gege,D., Galagni,J., Gandyra,S., Ginde,S., Gord,S., Goylette,M., Graham,L., Grand,Piere,S.,		

FEATURES	source	1. -209228 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /clone="RP3-61124" /clone.lib=RPCI-23 Female Mouse BAC"	Db
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misc_feature	15617. -134926 /note="assembly_fragment" clone_end:T7	Qy	173459 TCACTCTGGAGAGCTATGGAAAGGGCGCTGCAGGGCAATCATGGTGAAGGTCT
misc_feature	135026. contig of 100 bp 134927. 209228: contig of 74202 bp in length.	Qy	173399 TCATTCTGGAAAGCTATGAAAGGGCGCTGGCAGGGCAATCATGGTGAAGGTCT
BASE COUNT	56379 a 47110 c 47397 g 58042 t 300 others	Db	173567 882 CAGGATTCTCGATCCAAATGTGCTCCAGTCTGGTAGGCTGCCAGTCAGTCCACCTGC
ORIGIN		Db	173567 942 TCTCTATCTACTCTCATCACACACTGATGATCTCCCTATGATAGCTACACAGTACTACA
Query Match	Best Local Similarity 69.5%; Score 1243.4; Pred. No. 0; Matches 1452; Conservative 0; Mismatches 211; Indels 22; Gaps 6;	Db	173567 942 TCTCTATCTACTCTCATCACACACTGATGATCTCCCTATGATAGCTACACAGTACTACA
Qy	102 ACTRCACAGTCTCAGGCTTCCCCAATCCAGGGACTCGGGCGGGACTCGGGCGCTGTATGGA 161	Db	173567 942 TCTCTATCTACTCTCATCACACACTGATGATCTCCCTATGATAGCTACACAGTACTACA
Db	172746 AGTCCCTTCTCCCTGAGGCCTCCCGATCCGGGCTCTCTGAGGAACTGTATGGAA 172805	Db	173567 942 TCTCTATCTACTCTCATCACACACTGATGATCTCCCTATGATAGCTACACAGTACTACA
Qy	162 CGACATTTCACTCGATGCCGGAGGGAGGGAGGAGACATCAGCTCTCCCTGCACTGGCTG 221	Db	173567 1002 TGAAGGCACCATTCCTCTCACACACTAGAGGCCCTCATCCACGACATGACTCAAG
Db	172806 CAACAGTTCACTCGATGCTGAGAGGGAGACACGGCTGAGGCTGAGGCTGAGA 172860	Db	173567 1002 TGAAGGCACCATTCCTCTCACACACTAGAGGCCCTCATCCACGACATGACTCAAG
Qy	222 CAGGGAGAGAGACTCAACCAGGGAGACATCAGCTCTCCCTGCACTGGCTG 281	Db	173567 1062 AGGGGATGCCCTCTCACACACTAGAGGCCCTCATCCACGACATGACTCAAG
Db	172861 CATAGGAGATGACTCACTCAGGGGGTCACTGAGGCTGAGGCTGAGT 172920	Db	173567 1122 CGTACTGTAAATGATGATGAGATGACTGCTGCCCAGTCATGCTGACTCAAGT
Qy	282 CCGAGAGGGCCGCTCTGTGTTGAGATGATCATGGGGGAGGATCAATGT 341	Db	173567 1122 CGTACTGTAAATGATGATGAGATGACTGCTGCCCAGTCATGCTGACTCAAGT
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Qy	402 TGTACAGAGCTATTGAGTACAGGAGACATCAATGAGTGTAGAACCGGAATCT 461	Db	173567 1242 GAAGAACCTGAGACACACAGAGCTGAGCATGTTGAGGTTTGAGTGTCT
Db	173039 TGTAACAAAGCTGTGCAATACAGTGTAGACACCGAAATGT 173098	Db	173567 1302 GTGGGAACCTGGTACAGAGGGTACCTTGTGACCTCTCCAAATATGGATGAA
Qy	462 GCCCTGTGACTATGCTGTTGGGCCAGATAAGTGGCAGAGGAACCTGGCGAAA 521	Db	173567 1302 GTGGGAACCTGGTACAGAGGGTACCTTGTGACCTCTCCAAATATGGATGAA
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Qy	522 TGGGCCCTTGTGCAAGAACATGGAGATGGAGATGCTGGTGGAA 581	Db	173567 1362 GAAGGTGGCATGGAGGCTCTGGCCTACATCCACCGAGTATTCCCTCATGCTG
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Qy	582 ACCCTGAGAGCTTCCGAGAGGGGGAGAGATGGCGAGAATCTAACCGTAA 641	Db	173567 1422 TAACTCATGAGATCTGATGAGATGAGCTGAGGCTCTGGTCAATGAGCTG
Db	173219 ACCCTTGGAGACCTCTCCAGAACAGAGGGGAGGCTCAACCAT 173278	Db	173567 1482 TGTGCCTATCTGGAGAGATGAGGAGCAACTAGGACCTGTGAGGTCTGCCAACTCC
Qy	642 TCCATACAGGAGACATTGGAAGGGACACCCGACTCGGCCGAAATGAAACCT 701	Db	173567 1542 AGAGGTGTGGAGCATGGTGGGATGCCCTCCAAAGCAGGGGCTCTGGTGC
Db	173279 TCCATACAGGAGCTCTGGAGGGACACTGCAAGGCCCTGAATGGACCT 173338	Db	173567 1542 AGAGGTGTGGAGCATGGTGGGATGCCCTCCAAAGCAGGGGCTCTGGTGC
Qy	702 GACAAACACTCTGGCATGACTTCAACAGCTTACTCTGGAGGAAGCTCAAGAGA 761	Db	173567 1718 TCCACATGGAGGATCACCCCCCTGTACATAAAGTTATGAAAGAAAA
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Tue Sep 23 09:49:53 2003

us-09-840-704a-1.rge

Page 20

Db 174408 GAAGA 174412

Search completed: September 22, 2003, 18:28:21
Job time : 4407 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2003, 15:19:24 ; Search time 369 Seconds

Perfect score: 1789 (without alignments) 13087.519 Million cell updates/sec

Title: US-09-840-704A-1
Sequence: 1 gaatttcatctgtcgactgct.....aaaaaaaaaaaaaaaaaa 1789
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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RESULT 1
AAF69274
ID AAF69274 standard; DNA; 1789 BP.
XX
AC AAF69274;
XX
DT 18-APR-2001 (first entry)
XX
Human integrin-linked kinase DNA.
XX
KW antisense; integrin-linked kinase; hik; infection; tumour;
KW inflammation; ds.
XX
OS Homo sapiens.
XX
PN US6177273-B1.
XX
PD 23-JAN-2001.
XX
PP 26-OCT-1999; 99US-0428219.
XX
PR 26-OCT-1999; 99US-0428219.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM;
XX
DR WPI: 2001-137069/14.
XX
PT Novel antisense compounds capable of modulating expression of human
Integrin-linked kinase, useful for diagnosis, prophylaxis and treatment

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1787.4	99.9	1789 22 AAF69274	Human integrillin Human CDNA difference Human integrillin Human signalling protein Human breast tumor Lung cancer associated Nucleotide sequence Drosophila melanog
2	1787.4	99.9	1789 24 ABK84315	
3	1773.4	99.1	1786 18 AAT71716	
4	1771.4	99.0	1786 25 ACMA56473	
5	1693.4	94.7	1780 20 AAZ33623	
6	1352.6	75.6	1607 21 AAF18317	
7	1195.8	66.8	1359 22 AAF90197	
8	466.8	26.1	1820 23 ABL16569	

of diseases, e.g. tumors, associated with expression of the kinase -
 Example 13; Column 47-50; 40pp; English.

The present invention relates to an antisense compound 8 to
 30 bases in length targeted to the 5' untranslated (UTR) region,
 the coding region or the 3' UTR region human Integrin-linked
 kinase (hIK). The antisense oligonucleotides are useful for
 inhibiting the expression of human hIK in human cells or tissues
 in vitro. The oligonucleotides can be utilized for diagnostics,
 therapeutics for the treatment of diseases associated with
 the expression of hIK, prophylaxis, e.g. to prevent or delay infection,
 inflammation or tumor formation and as research reagent.

Sequence	1789	BP:	443 A;	488 C;	480 G;	378 T;	0 other;
Best Local Similarity	99.9%	Score	1787.4;	DB	22;	Length	1789;
Matches 1788;	Conservative	0;	Pred.	No	0;	Mismatches	1;
Matches 1788;	Indels	0;	Gaps				
Dy	1	GAATTCACTCTGACTGCTATAACCGGGAGTTCCCGGAGAAAGGATCCTGCAGCCGAGT	6				
Dy	1	GAATTCACTCTGACTGCTATAACCGGGAGTTCCCGGAGAAAGGATCCTGCAGCCGAGT	6				
Dy	61	CCGGAGGATAAAGCTTGGGTTCATCTCTCTCCCTGATCTCCAGTCTCAGCT	1				
Dy	61	CCGGAGGATAAAGCTTGGGTTCATCTCTCTCCCTGATCTCCAGTCTCAGCT	1				
Dy	121	TCCCCAAATCCAGGGACTCGGCCGGGACGGCTATGGACGCAATTTCAGTCAGTC	1				
Dy	121	TCCCCAAATCCAGGGACTCGGCCGGGACGGCTATGGACGCAATTTCAGTCAGTC	1				
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Dy	181	CGGGAGGSCAACGAGTGCCCTTGCGCTTGCGCTGGACAAACGGGAAACGAC	2				
Dy	241	CAAGGGAGCATATGGTTCTCCCCCTGCACTGGCTGGAGGGGGCTCTGCT	3				
Dy	241	CAAGGGAGCATATGGTTCTCCCCCTGCACTGGCTGGAGGGGGCTCTGCT	3				
Dy	301	GTGCTTGAGATGTTGATCATGGGGGACCGGATCAATGTAAATGAAACCCTGGATGAC	3				
Dy	301	GTGCTTGAGATGTTGATCATGGGGGACCGGATCAATGTAAATGAAACCCTGGATGAC	3				
Dy	361	ACCCCCTGCACTGGAGCCGCTATGGACACCCTGATATGTCAGAAAGGTTATGCG	4				
Dy	361	ACCCCCTGCACTGGAGCCGCTATGGACACCCTGATATGTCAGAAAGGTTATGCG	4				
Dy	421	TACAAGGGAGAATCAATGGCAATCAAGTGGCAATGAAACCGGAATGGCCCTGACATAGTCGCTGT	4				
Dy	421	TACAAGGGAGAATCAATGGCAATCAAGTGGCAATGAAACCGGAATGGCCCTGACATAGTCGCTGT	4				
Dy	481	TTTGGGCCCAAGATCAAGTGGCAAGGGACCTGGCCAAATGGGCCCTGACATAGTCGCTGT	5				
Dy	481	TTTGGGCCCAAGATCAAGTGGCAAGGGACCTGGCCAAATGGGCCCTGACATAGTCGCTGT	5				
Dy	541	TGTAACAAAGTATGGAGATGGCTGTGGACAAAGCCAGGAACTGGCCCTGAGAGAGCTCTC	6				
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Dy	601	CGAGAGGGGACACCCGGGACTCGGCCGAAATGGAAACCTGAAACAACACTCTGGATT	7				
Dy	601	CGAGAGGGGACACCCGGGACTCGGCCGAAATGGAAACCTGAAACAACACTCTGGATT	7				
Dy	661	TGAAGGGGAAATGGGGCAATGGAACTCTGGGAAATGGAAACCTGAAACAACACTCTGGATT	7				
Dy	661	TGAAGGGGAAATGGGGCAATGGAACTCTGGGAAATGGAAACCTGAAACAACACTCTGGATT	7				
Dy	721	GACTTCAAAAGCTTAACCTCTGACAGAGCTAACCGAGAAATCACTCTGGAGAGCTATGG	7				
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Dy	781	AGGGCCCTGGAGGGAAATGACATTCCTGTAAGGGTGTGAGGGTCAAGGAGCTGGAGT	8				

RESULT 2
ABK84315 ID ABK8
XX AC

XX
 XX DT 14-AUG-2002 (first entry)
 XX SQ Human cDNA differentially expressed in granulocytic cells #886.
 XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
 XX viral infection; parasitic infection; fungal infection; protozoal infection;
 XX sterile inflammatory disease; psoriasis;
 XX rheumatoïd rhinitis; glomerulonephritis; asthma; thrombosis;
 XX cardiac reperfusion injury; renal reperfusion injury; ARDS;
 XX adult respiratory distress syndrome; inflammatory bowel disease;
 XX Crohn's disease; ulcerative colitis; periodontal disease;
 XX granulocyte activation; chronic inflammation; allergy;
 OS Homo sapiens.
 XX PN WO200228999-A2.
 PD 11-APR-2002.
 XX PF 03-OCT-2001; 2001WO-US30821.
 XX PR 03-OCT-2000; 2000US-237189P.
 XX PA (GENE-) GENE LOGIC INC.
 XX PT Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -
 XX PS Claim 1; SEQ ID NO 886; 114pp; English.
 XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GA; preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 Note: The sequence data for this patent did not form part
 of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.

XX	SQ	Sequence 1789 BP; 443 A; 488 C; 480 G; 378 T; 0 other;
Query Match	99.9%	Score 1787.4; DB 24; Length 1789;
Best Local Similarity	99.9%	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches	1789; Conservative	
QY	1 GAATTCTATCTGTGACTGCTTACACGGAGTTCCCGAGAAGGATCCTGCAGCCGAGT	60
Db	1 GAATTCTATCTGTGACTGCTTACACGGAGTTCCCGAGAAGGATCCTGCAGCCGAGT	60
QY	61 CCCGAGGATAAGCTGGGTTACCTCTTCCCTGATCTGACTTCACAGCTCAGCT	120
Db	61 CCCGAGGATAAGCTGGGTTACCTCTTCCCTGATCTCCTCCCTGATCACTCCACAGCTCAGCT	120
QY	121 TCCCCATTCAGGGACTCGGCCGGAGGCTGTATGGAGCAATTCTACTCAGTG	180
Db	121 TCCCCATTCAGGGACTCGGCCGGAGGCTGTATGGAGCAATTCTACTCAGTG	180
QY	181 CGGGAGGCAACGCGTGTGGCTGGCTGGACACCGGAACGGACCTTCAC	240
Db	181 CGGGAGGCAACGCGTGTGGCTGGCTGGACACCGGAACGGACCTTCAC	240
QY	241 CAGGGGACCATCTGGTCTCCCTTCACTGGCTGGCTGTGCT	300
Db	241 CAGGGGACCATCTGGTCTCCCTTCACTGGCTGGCTGGCTGTGCT	300
QY	301 GTGGTTGAGTGTGATCTGGCTGGCTGGAGAAGCTGGATGTA	360
Db	301 GTGGTTGAGTGTGATCTGGCTGGCTGGAGAAGCTGGATGTA	360
QY	361 ACCCCCTGCACTGGCAGCCGTCATGGCACCTGATTTGAGCTTGAG	420
Db	361 ACCCCCTGCACTGGCAGCCGTCATGGCACCTGATTTGAGCTTGAG	420
QY	421 TACAAGGACAGCATCAATSGAGTGAACCGAATGCCCCGTGACTATGCTGT	480
Db	421 TACAAGGACAGCATCAATSGAGTGAACCGAATGCCCCGTGACTATGCTGT	480
QY	481 TTGGGGCCAGATACTGAGCTGGAGGACCTGCTGGCAATGGCCCTGTGAGTC	540
Db	481 TTGGGGCCAGATACTGAGCTGGAGGACCTGCTGGCAATGGCCCTGTGAGTC	540
QY	541 TGTAACTAGTGGAGATGAGCTGACAAGGCAAGGCCACCTGTGAGAGCTTC	600
Db	541 TGTAACTAGTGGAGATGAGCTGACAAGGCAAGGCCACCTGTGAGAGCTTC	600
QY	601 CGAGAGGGACCACCGCACTGGGCCCGAAATGGAAACACTCTGGATT	660
Db	601 CGAGAGGGACCACCGCACTGGGCCCGAAATGGAAACACTCTGGATT	660
QY	661 TGGAGGGGACCCGCACTGGGCCCGAAATGGAAACACTCTGGATT	720
Db	661 TGGAGGGGACCCGCACTGGGCCCGAAATGGAAACACTCTGGATT	720
QY	721 GACTTCAACAGCTRACTCTGTGAGAAGTCACTCTGGAGAGCTATGG	780
Db	721 GACTTCAACAGCTRACTCTGTGAGAAGTCACTCTGGAGAGCTATGG	780
QY	781 AAGGCGCTGGCAGGGCAATGACATTGTGTGAGGTGTGAAGTTCCAGACTGG	840
Db	781 AAGGCGCTGGCAGGGCAATGACATTGTGTGAGGTGTGAAGTTCCAGACTGG	840
QY	841 ACAAGGAGGAGGAGGACTCATGAGAGGTGTCCCCGGCTCAGATTCTGGATCCA	900
Db	841 ACAAGGAGGAGGAGGACTCATGAGAGGTGTCCCCGGCTCAGATTCTGGATCCA	900
QY	901 ATGGTCTCCAGTAGTGTGCTGCCAGTCCTCTCTACTCTCATC	960
Db	901 ATGGTCTCCAGTAGTGTGCTGCCAGTCCTCTACTCTCATC	960
QY	961 ACACAGTGGATGCCPATGATCCCTCTACATGAGGACCAATTCTGTC	1020

Db	961	ACACACTGGATGCCGTPATGGATCCCTTACATGTACTACATGAAAGCACCATAATTGTC 1020	FT	CDS	
Qy	1021	GTTGACCAAGACGCCAGGCTGTAAGTTTGCTTGGACATGGCAAGGGCATGGCTTCCTA 1080	FT	polyA_Signal	157..1512 /*tag= a
Db	1021	GTTGACCAAGACGCCAGGCTGTAAGTTTGCTTGGACATGGCAAGGGCATGGCTTCCTA 1080	FT		179..1154 /*tag= b
Db		W09723625-A1.	XX		
Qy	1081	CACACACTAGGCCCTATCCACACATAGCATAAGCGTAGTGAATGATTGAT 1140	XX		
Db	1081	CACACACTAGGCCCTATCCACACATAGCATAAGCGTAGTGAATGATTGAT 1140	XX		03 - JUL-1997.
Qy	1141	GAGGACATGACTGCCGAATTAGCATGGCTGATGAAAGTTCCTTCATGTCCTGGT 1200	XX		96WO-CA00760.
Db	1141	GAGGACATGACTGCCGAATTAGCATGGCTGATGAAAGTTCCTTCATGTCCTGGT 1200	XX		19-NOV-1996;
Db		(DEDHAR/)	XX		21-DEC-1995;
Qy	1201	CGCATGATGACCTGCCGTGGTAGGCCGAAGGCTGCGAAAGAACACA 1260	XX	PA	DEDHAR S. (HANN/)
Db	1201	CGCATGATGACCTGCCGTGGTAGGCCGAAGGCTGCGAAAGAACACA 1260	XX	PA	HANNIGAN G.
Db		Dedhar S., Hannigan G;	XX	PI	
Qy	1261	AACAGAGCTCAGCAGACATGGACATTTCAGAGCTCTCTGTTGGAAACCTGGTACCGG 1320	XX	WPI ; 1997-351062/32.	
Db	1261	AACAGAGCTCAGCAGACATGGACATTTCAGAGCTCTCTGTTGGAAACCTGGTACCGG 1320	XX	DR	P-PSDB; AAW18211.
Db		New isolated integrin-linked serine/threonine kinase - used to develop products to modulate cell growth, adhesion, migration and invasion, e.g. for treating cancer or inflammation	XX	PR	
Db		Claim 3; Fig 1a; 62pp; English.	XX	PT	
Qy	1321	GAGGTACCTTTGCTSACTCTTCAATATGAGATTGAAATGAAAGTGGCATGGAGGC 1380	XX	PT	
Db	1321	GAGGTACCTTTGCTSACTCTTCAATATGAGATTGAAATGAAAGTGGCATGGAGGC 1380	XX	PT	
Qy	1381	CTTCGGCCCTACCATCCCCACCGAGTATTCCCCTCATGGCTGTAAGTCATGATCTGC 1440	XX	PS	
Db	1381	CTTCGGCCCTACCATCCCCACCGAGTATTCCCCTCATGGCTGTAAGTCATGATCTGC 1440	XX	CC	cDNA clone Pla5 (AAT71716) codes for a serine/threonine kinase
Qy	1441	ATGAATGAAAGACCCCTGCAAGCGACCCAATTGACATGATTGCTCTTCATGAAAG 1500	XX	CC	(AAW18211) which is an integrin-linked kinase, designated ILK,
Db	1441	ATGAATGAAAGACCCCTGCAAGCGACCCAATTGACATGATTGCTCTTCATGAAAG 1500	XX	CC	that can be used to modulate cell growth, adhesion, migration and invasion. It was isolated from a human placental cDNA library
Qy	1501	ATGCAAGCAAGTAGGACTGAAAGTCCTTGCTGAACTCCAGAGTGTGGACATGGT 1560	XX	CC	using a partial cDNA, Bari-9, that had been mapped to
Db	1501	ATGCAAGCAAGTAGGACTGAAAGTCCTTGCTGAACTCCAGAGTGTGGACATGGT 1560	XX	CC	cytoplasmic domain. The ILK chromosomal locus has been mapped to
Qy	1561	TGGGGAAATGACCTCCCAAAGCAGCAGGGCTCTGGTGCCTCCCCCTCCAGTCAT 1620	XX	CC	1p11, a region implicated in a subset of breast carcinomas.
Db	1561	TGGGGAAATGACCTCCCAAAGCAGCAGGGCTCTGGTGCCTCCCCCTCCAGTCAT 1620	XX	CC	ILK nucleic acids (including antisense) can be used in gene therapy to inhibit tumours, chronic inflammatory disease, arthritis, osteoporosis and cardiovascular disease, and can also be used as diagnostics to screen biopsy samples.
Qy	1621	GTTACTACCCAGCTGGGTCCATCCCCATCCCTACCACTGTCGCCAGAGGG 1680	XX	SQ	Sequence 1786 BP; 443 A; 487 C; 479 G; 377 T; 0 other.
Db	1621	GTTACTACCCAGCTGGGTCCATCCCCATCCCTACCACTGTCGCCAGAGGG 1680	XX	Query Match	99.1%; Score 1773; DB 18;
Qy	1681	GGCGGGCTCAGAGCTTGTCACTTGCCACATGGTCTCCACATGGGGATCGCC 1740	XX	Best Local Similarity	99.8%; Pred. No. 0;
Db	1681	GGCGGGCTCAGAGCTTGTCACTTGCCACATGGTCTCCACATGGGGATCGCC 1740	XX	Matches 1786; Conservative 0; Mismatches 0; Indels 3; Gaps 1;	
Qy	1741	CGGCCCTGTACACATAAGTTTATTATGAAAAA.....AAAAA 1789	XX	Qy	1 GAATTCATCTCTGCTGACTGCTGTTGCTGAGCTTCATCCCTGGTCAAGCTGGTCTGGGT 60
Db	1741	CGGCCCTGTACACATAAGTTTATTATGAAAAA.....AAAAA 1789	XX	Db	1 GAATTCATCTCTGCTGACTGCTGTTGCTGAGCTTCATCCCTGGTCAAGCTGGTCTGGGT 60
RESULT 3			Db	61 CCCGAGGATAAAGCTGGTCACTCTCTGGTCAAGCTGGTCTGGGT 120	
AAT71716	ID	Human integrin-linked kinase (ILK) cDNA.	Db	61 CCCGAGGATAAAGCTGGTCACTCTCTGGTCAAGCTGGTCTGGGT 120	
	XX		Qy	121 TCCCCAATCCAGGGGACTCGGCCGGAGCTGGTATGGACATTTCACTAGTCAGTC 180	
AAT71716;	AC	Integrin-linked kinase; ILK; serine/threonine kinase; cell growth;	Db	121 TCCCCAATCCAGGGGACTCGGCCGGAGCTGGTATGGACATTTCACTAGTCAGTC 180	
	XX	cell adhesion; cell migration; inhibitor;	Qy	1241 CAGGGGGACATCGCTTCCTCCCTTCGACTCGGCCGCTCTGC 300	
		gene therapy; diagnosis; cancer; leukaemia; tumour; inflammation;	Db	1241 CAGGGGGACATCGCTTCCTCCCTTCGACTCGGCCGCTCTGC 300	
		arthritis; osteoporosis; cardiovascular disease; ss.	Qy	181 CGGGGGGAAACGCACTGCTGCTGGTCAACAGCGAGCACTCAAC 240	
		OS Homo sapiens.	Db	301 GTGGTTGAGATGTTGATCATCGGGGGCACGGATCAATGTAATAAACCGTGGGATGAC 360	
	XX	Location/Qualifiers	Qy	361 ACCCCCCCTGCACTCGCAGGCTATGGACACCCGTGATATTGACAGAAGCTATTCGAG 420	
	FH				

for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at www.uspto.gov/nvl/simone.htm?m=1&f=1&g=1&h=1&s=1&t=1

KW	Expressed sequence tag; EST; human; breast; cancer; gene therapy;	Db	494 CAGAGGACCTGGTGCACATGGGCCCTTCAGCATCTGTAACAGATAAGGAGATGC 553
KW	treatment; tumour; cytostatic; medicament; SE.	Qy	563 CTGTGCAAAAGCCAGCAGCACCCCTGAGAGCTTCTCCAGAGGGGCGCAGAAGATGG 622
OS	Homo sapiens.	Db	564 CTGIGACAAGCCAGCAGCACCCCTGAGAGCTTCTCCAGAGGGGCGCAGAAGATGG 613
XX		PN	DE19813819-A1.
XX		PD	23-SEP-1999.
XX		PR	20-MAR-1998; 98DE-1013839.
XX		PR	20-MAR-1998; 98DE-1013839.
PA	(META-) METAGEN GES GENOMFORSCHUNG MBH.	PA	XX
PT	Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;	PT	XX
XX	WPI: 1999-528881/45.	PS	XX
DR	Human nucleic acid sequences and protein products from tumor breast tissue, useful for breast cancer therapy	DR	XX
CC	Claim 3; 94; 188pp; German.	CC	XX
CC	This invention describes novel human nucleic acid sequences from tumor breast tissue which have cytotoxic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer. AA233611-Z48617 represents expressed sequence tags described in the method of the invention.	CC	XX
SQ	Sequence 1780 BP; 427 A; 489 C; 492 G; 372 T; 0 other;	SQ	XX
Query Match 94-71; Score 1693 4; DB 20; Length 1780;			
Best Local Similarity 99.1%; Pred: No. 0; Matches 1745; Conservative 0; Mismatches 11; Indels 5; Gaps 4;			
Qy	24 ACGGGAGTCCCGGAGAACGATCCCTCGAGCCGAGTCCGGAGATAAGCTTGGGTC 83	Qy	803 ATATTCTGTGAAGTGCTGAGACTTGAGACTTGAGATCTGGATCTGACTTCAA 733
Db	14 ACGGTGATTCGGCCGAGAACGATCCCTCGAGCTCCAGATAAGCTTGGGTC 73	Db	804 ATGAGAGTGTCCCCGGCTCAGGATTCTCGATCCAAATGTTGTCAGGTGCTAGGT 913
Qy	84 ATCCCTCTCTCCCTGGATCAC-TCCACAGTCTCAGGCTCCAAATCCAGGGACTCGG 142	Qy	743 TGACGAGCTAACGAGAATCTGAGAGCTTGAGGTTGAGACTGGATCAAGGA 793
Db	74 ATCCCTCTCTCCCTGGAGCCCGAGTCCCTGAGCTCCAGATAAGCTTGGGTC 133	Db	794 ATGAGAGTGTCCCCGGCTCAGGATTCTCGATCCAAATGTTGTCAGGTGCTAGGT 922
Qy	143 CGCGGAGACGGCTATGACCCACATTTCAGTCAGTGCAGGGAGGCAACCGAGTGGC 202	Qy	893 CCCTCTACATGTACTACATGACCTGAGGATTTCTCGATCCAAATGTTGTCAGGT 1042
Db	134 CGCGGAGACGGCTATGACCCACATTTCAGTCAGTGCAGGGAGGCAACCGAGTGGC 193	Db	974 CCCTCTACATGTACTACATGACCTGAGGACCAATTTGTCGTGACCAGGCCAGGT 1033
Qy	203 TTGCGCTGTGCTGGACACACCGGAGACGCCCTCACCCAGGGAGCATGGCTCT 262	Qy	1043 AGTTGCTTGGACATGCAAGGGGATGGCTCTCTACACACTAGAGGCCCTCATCC 1102
Db	194 TTGCGCTGTGCTGGACACACCGGAGACGCCCTCACCCAGGGAGCATGGCTCT 253	Db	1034 AGTTGCTTGGACATGCAAGGGGATGGCTCTCTACACACTAGAGGCCCTCATCC 1093
Qy	263 CCCCTCTGGACACACCGGAGACGCCCTCACCCAGGGAGCATGGCTCT 322	Qy	1103 CACGACATGCACTCATAGCGTAGTTAATGATGATGAGCATGTCGCCGATTA 1162
Db	254 CCCCTCTGGACACACCGGAGACGCCCTCACCCAGGGAGCATGGCTCT 313	Db	1094 CACGACATGCACTCATAGCGTAGTTAATGATGATGAGCATGTCGCCGATTA 1153
Qy	323 GGGGGCAGCGATCAATGTAATGAAACGGTGGGATGACCCCTGCACTGGAGCCA 382	Qy	1163 GCATGGCTGATGTCAGGTCCTTCACATGTCCTCGTGGCATGATGACCTGCTGG 1222
Db	314 GGGGGCAGCGATCAATGTAATGAAACGGTGGGATGACCCCTGCACTGGAGCCA 373	Db	1154 GCATGGCTGATGTCAGGTCCTTCACATGTCCTCGTGGCATGATGACCTGCTGG 1213
Qy	383 GTCTGGACACCGTGTATGTCAGAGCTATGCACTGAGGAGACCTCAACCGGAGA 442	Qy	1223 TAGCCCCGAAGCTCTGAGAGAACGACCTGAGAGAACACAAAGAGGCTCAGCAGCATGT 1282
Db	374 GTCTGGACACCGTGTATGTCAGAGCTATGCACTGAGGAGACCTCAACCGGAGA 433	Db	1214 TAGCCCCGAAGCTCTGAGAGAACGACCTGAGAGAACACAAAGAGGCTCAGCAGCATGT 1273
Qy	443 TGAATGACACCGGAATGTGCCCTGCACTATGCCCTGTTGGGCCAACATCAAGTG 502	Qy	1283 GGAGTTTGCACTGGCTCTGGGAACCTGGTACGGAGGATCTCCCTTGCTGACCT 1342
Db	434 TGAATGACACCGGAATGTGCCCTGCACTATGCCCTGTTGGGCCAACATCAAGTG 493	Db	1274 GGAGTTTGCACTGGCTCTGGGAACCTGGTACGGAGGATCTCCCTTGCTGACCT 1333
Qy	503 CAGAGGACCTGGGCAATGGGCCCTTGCACTGAGAATGAGAGATGGAGAGATG 562	Qy	1343 CCAATTTGGAGATTGATGAGGTCGATGGCTGAGAGATGGCTGAGGAGATGG 1402
Db	1573 GCAGCAGGCCCTGGTGCCTCCAGGCTCCAGTCAGGCTGAGGAGATGGCTGAGG 1632	Db	1393 GATTTCCCTCATGTTGAGCTCATGAGATCTGAGATGAGGACCTGCAAG 1452
Qy		Qy	1463 GACCCAAATTGACATGATGTCGCTCATCCCTGAGAGATGGCTGAGGAGATGG 1522
Db		Db	1453 GACCCAAATTGACATGATGTCGCTCATCCCTGAGAGATGGCTGAGGAGATGG 1512
Qy		Qy	1523 AGTCCTGCTGACTCCAGGGCTCGGACATCTGGTGGGGATGACCTCCCAA 1582
Db		Db	1513 AGTCCTGCTGACTCCAGGGCTCGGACATCTGGTGGGGATGACCTCCCAA 1572
Qy		Qy	1583 GCAGCAGGCCCTGGTGCCTCCAGTCAGGCTGAGGAGATGGCTGAGGAGATGG 1641

		SQ	Sequence 1607 BP; 435 A; 427 C; 416 G; 322 T; 7 other;
Qy	1642 CCATCCCCCTCCCATCCCTTACCACTGTG - CGCAAGGGGGCTCAGAGCTTTGT 1699	Query Match	75.6%; Score 1352.6;
Db	1633 CCATCCCCCTCCCATCCCTTACCACTGTG - CGCAAGGGGGCTCAGAGCTTTGT 1692	Best Local Similarity	99.5%; Pred. No. 0;
Qy	1700 CACTGCCACATGGTGTCTCCAAACATGGGGGATCAGCCCGCTGTACAATAAAGT 1759	Matches 1375; Conservative	2; Mismatches 2; Indels 3; Gaps 2;
Db	1693 CACTGCCACATGGTGTCTCCAAACATGGGGGATCAGCCCGCTGTACAATAAAGT 1752	Qy	411 GCTATGCGATCACAGGCAGACATCAATGCGATGAAACACCGGAATGTGCCCTGC 470
Db	1750 TTATTATGAAAAAAA 1780	Db	186 GCTATGCGATCACAGGCAGACATCAATGCGATGAAACACGGGAATGTGCCCTGC 245
Qy	1753 TTATTATGAAAAAAA 1773	Qy	471 CTATGCCCTGGCAAGATCAAGTGGCAAGGACCTGGTCAAATGGGCCCT 530
Db	1751 TTATTATGAAAAAAA 1773	Db	246 CTATGCCCTGGCAAGATCAAGTGGCAAGGACCTGGTCAAATGGGCCCT 305
RESULT 6			
AAFI18317	AAFI18317 standard; DNA; 1607 BP.	Qy	531 TGTCAGCATCTGTACAAGTATGGAGATGCCCTGGACAAAGCCAAGGCCACCCCTGAG 590
ID	AAFI18317	Db	306 TGTCAGCATCTGTACAAGTATGGAGATGCCCTGGAAAGCCAAAGGCCACCCCTGAG 365
XX		Qy	591 AGAGCTTCTCGAGAGCGGGCAGAGAATGGCCAGAACCTCAACCGPATTCATACAA 650
AC	AAFI18317;	Db	366 AGAGCTTCTCGAGAGCGGGCAGAGAAGTGGCCAGAACCTCAACCGPATTCATACAA 425
XX	14-MAR-2001 (first entry)	Qy	651 GGACACATTGGAGGGACCACCGACTGGCCGAATGGAACCCCTGAAACAAACA 710
DE	Lung cancer associated polynucleotide sequence SEQ ID 336.	Db	426 GGACACATTGGAGGGACCACCGACTGGCCGAATGGAACCCCTGAAACAAACA 485
XX		Qy	711 CTCTGGCATGGCTAACAGCTTAACCTCTGAGAACCTCAACAGAGATACTCTGG 770
KW	Human; lung cancer associated protein; neuroprotective; cytostatic;	Db	486 CTCTGGCATGGCTAACAGCTTAACCTCTGAGAACCTCAACAGAGATACTCTGG 545
KW	cardioactive; immunomodulatory; muscular active; pulmonary;	Qy	771 AGAGCTTATGGAAAGGCCCTGGAGGGCAATGACATTGCTGAGGTGTGAAGGTTCG 830
KW	gastrointestinal; nephrotrropic; antinefrective; vulnery;	Db	546 AGAGCTTATGGAAAGGCCCTGGAGGGCAATGACATTGCTGAGGTGTGAAGGTTCG 605
KW	antibacterial; nephrotrropic; antiinfective; gynecological;	Qy	831 AGACTGGAGTACAAGGAAGCAGGAGCTCAATGAAGAGTGTCCCCTGGCTCAGGATT 890
KW	anti bacterial; diagnosis; neural disorder; immune disorder; reproductive;	Db	606 AGACTGGAGTACAAGGAAGCAGGAGCTCAATGAAGAGTGTCCCCTGGCTCAGGATT 665
KW	proliferative disorder; wound healing; infectious disease; ds.	Qy	891 CTCGGATCCAAATGTGCTCCCTGGCTAGTGTCAAGTCCACCTCTGCTCATCC 950
XX	Homo sapiens.	Db	666 CTCGGATCCAAATGTGCTCCCTGGCTAGTGTCAACCTCTGCTCATCC 725
OS		Qy	951 TACTCTCATCACACTGGATGCCCTATGGATCCCTCAATGACTACATGAAAGGCAC 1010
PN	WO200055180-A2.	Db	726 TACTCTCATCACACTGGATGCCCTATGGATCCCTCAATGACTACATGAAAGGCAC 785
XX		Qy	1011 CAATTCCTGCTGAGGACATGCTGGCCAGGCTGTGAAGTGTGCTTGGCATGGGGCAT 1070
PD	21-SEP-2000.	Db	786 CAATTCCTGCTGAGGACATGCTGGCCAGGCTGTGAAGTGTGCTTGGCATGGGGCAT 845
XX		Qy	1071 GGCCCTTCCTACACACACTAGGCCCCCATCCACGACATGCACTCAATAGCCGTAGTGT 1130
PF	08-MAR-2000; 2000WO-US05918.	Db	846 GGCCCTTCCTACACACACTAGGCCCCCATCCACGACATGCACTCAATAGCCGTAGTGT 905
XX		Qy	1131 AATGATTGATGAGGGACATGCTGGCCAGGCTGTGAAGTGTGCTTGGCATGGGGCAT 1190
PR	12-MAR-1999; 99US-0124270.	Db	906 AATGATTGATGAGGGACATGCTGGCCAGGCTGTGAAGTGTGCTTGGCATGGGGCAT 965
XX	(HUMA-) HUMAN GENOME SCI INC.	Qy	1191 ATGTCCTGCTGAGGCTACCTCTGCTGAGGCTGTGAAGTGTGCTTGGCATGGGGCAT 1250
PA	(ROSE/) ROSEN C A.	Db	966 ATGTCCTGCTGAGGCTACCTCTGCTGAGGCTGTGAAGTGTGCTTGGCATGGGGCAT 1025
XX	Ruben SM;	Qy	1251 TGAAGACACAAAGACGACATGGAGGACTGTGGAACTTGGCTGCTTGGGGAACT 1310
PI		Db	1026 TGAAGACACAAAGACGACATGGAGGACTGTGGCTGCTTGGGGAACT 1085
XX	WPI: 2000-587514/55.	Qy	1311 GGTGACACGGGAGGTACCCCTGGCTGACCTCTGGCTGAGGATGGATGAGGTGGCC 1370
DR	P-PSDB; AAB58441.	Db	1086 GGTGACACGGGAGGTACCCCTGGCTGACCTCTGGCTGAGGATGGATGAGGTGGCC 1145
XX		Qy	1371 ATTGGAAAGGGCTTCGGCTTACCATCCACAGGTTTCCCTCATGTGTAAAGCTCAT 1430
PT	Lung cancer associated gene sequences, referred to as lung cancer	Db	1146 ATTGGAAAGGGCTTCGGCTTACCATCCACAGGTTTCCCTCATGTGTAAAGCTCAT 1205
PT	associated proteins and polynucleotide sequences, their agonists, and		
PT	antagonists may have neuroprotective; cytostatic; cardioactive;		
PT	immunomodulatory; muscular active; general; pulmonary; gastrointestinal		
PT	general; nephrotrropic; antiinfective; gynecological; or antibacterial		
PT	activity. The invention also includes antibodies specific for the		
XX	protein or polynucleotide sequences. The lung cancer associated		
XX	polynucleotide sequences may be used for detection of lung cancer,		
XX	chromosome identification, as chromosome markers, and for numerous other		
XX	diagnostic or research purposes. The proteins may be used to treat		
CC	disorders such as neural, immune, muscular, reproductive,		
CC	gastrointestinal, pulmonary, cardiovascular, renal, and proliferative		
CC	disorders. The proteins may also be used in the treatment of wounds and		
CC	infectious diseases. Polynucleotide sequences AAF18424 - AAF1843 and		
CC	peptide AAB58549 are used in the course of the invention for the		
CC	identification and characterisation of the polynucleotide and protein		
CC	sequences.		

QY 1431 GAAAGATCTGCTGAATGAAACCCCTGCAAAAGCACCCTAAATTGACATGATGTCCTAT 1490
 CC proliferation, adhesion or migration of cells, especially tumour cell
 CC invasion, and is overexpressed in highly invasive cancer cells. ILK-2
 CC polynucleotides are used for recombinant expression of the corresponding
 protein; as a source of diagnostic/therapeutic primers, probes and
 CC antisense sequences; and for treating diseases involving expression of
 CC ILK-2, particularly cancer and especially prevention or inhibition of
 CC metastases, when incorporated into a gene therapy vector. ILK-2
 CC polypeptides are used to raise antibodies, and also to screen for
 CC agents (potential anticancer agents) that inhibit ILK-2.
 XX Sequence 1359 BP; 357 A; 337 C; 364 G; 301 T; 0 other;

QY 1611 CTCCAGTCATGTTACTACCCAGCC-TGGGGTCCATCCCTTCCCCATCCCTTACACTG 1659
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 1386 CTCCAGTCATGTTACTACCCAGCC-TGGGGTCCATCCCTTCCCCATCCCTTACACTG 1445
 QY 1670 TG-CGCAAGGGGGGGCTCAGACTTGTACTTGCAATTAAGTTTATGAAAAAAA 1727
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 1446 TKGNCNCCAAGGAGGGGGCTCAGACTTGTACTTGCAATCCCTTACACTG 1505
 QY 1728 GGAGGGATCAGCCGCCCTGTCAATAAGTTTATGAAAAAAA 1787
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 1506 GGAGGGATCAGCCGCCCTGTCAATAAGTTTATGAAAAAAA 1565
 QY 1788 AA 1789
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 1566 AA 1567
 RESULT 7

ID AAF90197 standard; DNA; 1359 BP.

XX AAF90197:
 AC
 XX DT 06-AUG-2001 (first entry)

DE Nucleotide sequence of a human integrin-linked kinase (ILK-2).

XX Human; integrin-linked kinase; ILK-2; serine kinase; threonine kinase; cell proliferation; cell adhesion; cell migration; tumour; cancer; ss; OS Homo sapiens.

XX Key Location/Qualifiers
 FT 1..1359 /*tag= a product="integrin-linked kinase (ILK-2)"
 FT
 FN WO200138542-A1.

XX PD 31-MAY-2001.

XX PF 22-NOV-2000; 2000WO-FR03247.

XX PR 23-NOV-1999; 99FR-001411.

XX PA (CNRS) CNRS CENT NAT RECH SCI. (REPUR-) CENT RECH PUBLIC SANTE-CRP-SANTE.

XX PI Kieffer N, Melchior C, Janji B;

XX DR WPI, 2001-367694/38.

XX PA P-PSDB; ARB84202.

PT New integrin-linked kinase-2 polypeptides and poly nucleotides, useful for gene therapy of cancer -

PT for gene therapy of cancer -

XX PS Claim 1; Page 51, 61pp; French.

XX CC The present sequence encodes a human integrin-linked kinase (ILK-2). ILK-2 is a serine/threonine kinase that is implicated in control of

CC proliferation, adhesion or migration of cells, especially tumour cell
 CC invasion, and is overexpressed in highly invasive cancer cells. ILK-2
 CC polynucleotides are used for recombinant expression of the corresponding
 protein; as a source of diagnostic/therapeutic primers, probes and
 CC antisense sequences; and for treating diseases involving expression of
 CC ILK-2, particularly cancer and especially prevention or inhibition of
 CC metastases, when incorporated into a gene therapy vector. ILK-2
 CC polypeptides are used to raise antibodies, and also to screen for
 CC agents (potential anticancer agents) that inhibit ILK-2.
 XX Sequence 1359 BP; 357 A; 337 C; 364 G; 301 T; 0 other;

QY 157 ATGGACGACTTTCACTCTAGTGGGGAGGGCAACGAGCTGGCTTCCCTGCGCTG 216
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 1 ATGGACGACTTTCACTCTAGTGGGGAGGGCAACGAGCTGGCTTCCCTGCGCTG 60
 QY 217 GACACACGGAGAACCTCAACAGGGAGCATAGCTTCTCCCTTCACTGG 276
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 61 GACAACACAGAAACGACTCACTGAGGATGATCATGCTTCTCCCTTCACTGG 120
 QY 277 GCCTGGCGAGGGGGCGCTGCTGCTGTTGAGATGTGATCATCGGGGACGGTC 336
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 121 GCCTGGCGAGAGGGCGCTGCTGCTGTTGAGATGTGATCATGAGGGAGCATGTC 180
 QY 337 AATGAAATGACCGGGGGTAGACACCCCTGCACTCTGCAAGCCAGTCAGCACCGT 396
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 181 ATGTTGATGATGTTGGGGTAGACCCCTGCACTCTGCAAGCCAGTCAGCACCGT 240
 QY 397 GATATGTTAGAGACGCTATTGCACTAACAGGAGCATCATGCTGAGTGTGACACGG 456
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 241 GACATGTCAGAAGCTGTTGCAATACAGAGCTGACATCATGCTGAGTGAATGGG 300
 QY 457 AATGTCCTCTGACTATGCTGTTGGGCCAAGATCAAGTGGAGGACCTGTTG 516
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 301 AATGTCCTCTGACTATGCTGTTGGCTCAAGACAGGAGCTGCAAGGAGCTGTTG 360
 QY 517 GCAAATGGGCCCTGTAGCATCTGTAACAGATGAGAGATGCCCTGAGACAAGGCC 576
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 361 GCTAAGGGCTCTGTCAGCATCTGTAACAGATGAGAGATGCCCTGAGACAAGGCC 420
 QY 577 AAGGACCCCTGAGAGCTCTCGAGAGCAGGGCCAGAGAGATGGCCAGAATCTCAAC 636
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 421 AAGGCACCCCTTAGAGAGCTCTGGAGAACAGGGAGAGATGGCCAGAATCTCAAC 480
 QY 637 CGTATTCATACAGGACATCTGGAGGGGACCACCCGCAGCTGGCCCCGAATGGA 696
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 481 CGTATTCATACAGGACATCTGGAGGGGACCACTGTCAGCTGGCCCCGAATGGA 540
 QY 697 ACCCTGAAACACACTCTGGCATTCACCTAACACAGCTTACTCTGAGGAAGCTC 756
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 541 ACCCTGAAACACACTCTGGCATTCACCTAACACAGCTCAGCTGGCCCCGAATGGA 600
 QY 757 GAGATCACTCTGGAGGCTATGGAGGAGCGCTGGCACTGGCAAGTGTGAG 816
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 601 GAGATCACTCTGGAGGAGCTATGGAGAAGGGCGCTGGCAAGTGTGAG 660
 QY 817 GTGCTGAGGTTCTGAGACTACAGGAGGAGGACTCTAATGAAAGAGTGTCCC 876
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 661 GTGCTGAGGTTCTGAGACTACAGGAGGAGCTCTAATGAAAGAGTGTCCC 720
 QY 877 CGCTCTGAGGTTCTGCAATGCTCCAGTGTGCTGGCTGCTCCAGTCTCCA 936
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 721 CGCTCTGAGGTTCTGCAATGCTCCAGTGTGCTGGCTGCTCCAGTCTCCA 780
 QY 937 CCTGCCTCTACTCTACTCATCACACCTGGATGCCGATGGTCCCTACATGTA 996
 CC Query Match 66.8%; Score 1195.8; DB 22; Length 1359;
 CC Best Local Similarity 92.5%; Pred. No. 0;
 CC Matches 1257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 CC Db 781 CCAGCTCCACCCACCTTACACACTGGATGCCATATGGTCTCTACATGTA 840
 QY 997 CTACATGAAAGGCCACCAATTGCTGCTGACCAAGGCCAGCTGAAAGTTGCTTGGAC 1056

RESULT 10
 AAA78148 standard; cDNA: 330 BP.
 XX
 AC AAA78148;
 XX DT 14-NOV-2000 (First entry)
 DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:435.
 XX Human Colon tumour polypeptide; tumour antigen; cancer; vaccine;
 KW immunotherapy; diagnosis; progression; ss.
 XX OS Homo sapiens.
 XX PR WO2000037643-A2.
 XX PD 29-JUN-2000.
 XX PF 23-DEC-1999; 99WO-US30909.
 XX PR 23-DEC-1998; 98US-0221298.
 PR 02-JUL-1999; 99US-0347996.
 PR 22-SEP-1999; 99US-0401064.
 PR 19-NOV-1999; 99US-0444442.
 PR 02-DEC-1999; 99US-0454150.
 XX PA (CORIXA CORP.
 PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
 PI Wang T, Yuqiu J;
 DR WPI: 2000-442671/38.
 XX PT New colon tumor polypeptides used to inhibit the development of cancer,
 PT especially colon cancer, and for diagnosing and monitoring the
 PT progression of the cancer -
 XX PS Claim 1; Page 216; 229pp; English.
 CC Sequences AAA77722-A78199 represent 478 cDNAs encoding proteins or
 CC portions of proteins which are associated with human colon tumours.
 CC The invention also specifically discloses 8 human colon tumour proteins
 CC (AAB11897-B11904). The nucleic acids, the polypeptides they encode, and
 CC antigen presenting cells (APCs, preferably dendritic cells) expressing
 CC such polypeptides may be used in vaccines that target tumour cells,
 CC especially colon tumour cells, thereby inhibiting the development of
 CC cancer. T-cells specific for the polypeptide expressed by the APC are
 CC used to remove tumour cells from biological samples, especially blood or
 CC fractions thereof. The sample or the isolated T-cells specific for the
 CC polypeptide can then be used to inhibit cancer development CD4+ and/or
 CC CD8+ T-cells from a patient may be incubated with a polypeptide or
 CC nucleic acid of the invention, or an APC expressing such a polypeptide,
 CC to cause the proliferation of specific T-cells. The T-cells can be
 CC cloned and then administered back to the patient to inhibit cancer
 CC development. Nucleic acids encoding the polypeptides and antibodies
 CC against the polypeptides may be used to determine the expression level
 CC of a tumour protein of the invention, and therefore to determine whether
 CC cancer cells are present. Such diagnostic methods may also be used to
 CC monitor the progression of a cancer by repeating the processes at time
 CC intervals, and comparing the current result to previous results. The
 CC present sequence represents a cDNA encoding a human colon tumour
 CC polypeptide.
 XX Sequence 330 BP; 76 A; 89 C; 83 G; 82 T; 0 other;
 SQ Query Match Score 328.4; DB 21; Length 330;
 Best Local Similarity Pred. No. 3.9e-82;
 Matches 99.7%; Mismatches 0; Indels 0; Gaps 0;
 CC 996 ACTACATGAAAGCACCATTCTGTCTGACAGCCAGGCTGTAAGTTGCTTGGAA 1055
 CC The present invention describes colon tumour associated proteins (I) and
 CC the polynucleotides (II) that encode them. (I) have cytostatic activity.
 CC (I) and (II) can be used in gene therapy and vaccine production. (I) and
 CC (II) may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate colon tumour associated protein (ICAP)
 CC expression, such as colonic cancer. For example, (I) and (II) may be
 CC used to treat disorders associated with decreased expression by
 CC rectifying mutations or deletions in a patient's genome that affect the
 CC activity of ICAPS by expressing inactive proteins or to supplement the

patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (III) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridization assays to detect and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28660 to AAI29512 and AAM2494 to AAM4523 represent nucleotide and amino acid sequences given in the exemplification of the present invention.

Sequence 330 BP; 76 A; 89 C; 83 G; 82 T; 0 other;

Query Match 18.4%; Score 328.4; DB 22; Length 330; Best Local Similarity 99.7%; Pred. No. 3.9e-82; Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 996 ACTACATGAAGGCCAACATTGCTGTCTGGACAGAGCCAGCAGTCAGTGTGAAAGTTGCTTGGA 1055

Db 330 ACTACATGAAGGCCAACATTGCTGTCTGGACAGAGCCAGCAGTCAGTGTGAAAGTTGCTTGGA 271

QY 1056 CATGCAAGGSGCATGCCTTCTACACACTAGAGCCCTCATCCACACAGACTAGTGCCTGCACT 1115

Db 270 CATGGCAAGGGCATGCCTTCTACACACTAGAGCCCTCATCCACACAGACTAGTGCCTGCACT 211

QY 1116 CAATACCGCTGTGTATGATGATGAGGAGATGACTGCCCCAATTAGCTTGGCTGATGT 1175

Db 210 CAATAGCCGTGTGTATGATGATGAGGAGATGACTGCCCCAATTAGCTTGGCTGATGT 151

QY 1176 CAAGTCTCTTCCAAATGCTCTGGTGCATGTATGACCTCTGGTAGGCCCGGAAGC 1235

Db 150 CAAGTCTCTTCCAAATGCTCTGGTGCATGTATGACCTCTGGTAGGCCCGGAAGC 91

QY 1236 TCTGCAAGAGGAGCTGAGACACAGACAGGCTCAGCACATGGAGTTTGCACT 1295

Db 90 TCTGCAAGAGGAGCTGAGACACAGACAGGCTCAGCACATGGAGTTTGCACT 31

QY 1296 GCTTCCTGTGGAACTGGTGAACGACGGGAGGT 1325

Db 30 GCTTCCTGTGGAACTGGTGAACGACGGGAGGT 1

RESULT 12
ABZ33072/C
ID ABZ33072 standard; cDNA; 330 BP.

AC ABZ33072;
XX DT 30-JAN-2003 (first entry)

XX DE Human colon tumour cDNA clone 32010 SEQ ID NO:435.
XX KW Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
KW tumour; immune response; immunostimulant; cytostatic; vaccine;
KW gene; ss.
XX OS Homo sapiens.

XX PD 24-OCT-2002.
XX PP 09-APR-2002; 2002WO-US11475.
XX PR 10-APR-2001; 2001US-0831263.
PR 03-AUG-2001; 2001US-0922217.
PR 19-DEC-2001; 2001US-0025380.

PA (CORI-) CORIXA CORP.

XN Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;

PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD;

PI Skeiky YAW, Fanger GR, Vedvick TS, Carter D;

XX DR WPI; 2003-067548/06.

XX New polynucleotide, useful for the preparation of a composition for stimulating an immune response against, or treating, cancer - Example 1; Page 255-256; 537pp; English.

XX The present invention describes compounds (1) for the immunotherapy and diagnosis of colon cancer. Also described: (1) a method for detecting the presence of cancer in a patient; (2) a method for stimulating and/or expanding T cells specific for a tumour protein; (3) an isolated T cell population comprising T cells prepared by the method of (2); (4) a method for stimulating an immune response in a patient; (5) a method for treating cancer in a patient; and (6) a method for inhibiting the development of cancer in a patient. (1) have immunostimulant and cytotoxic activities and can be used in vaccines. ABB3264 to ABZ33725 and ABP5343 to ABP53391 represent human colon cancer/tumour related sequences used in the exemplification of the present invention.

XX Sequence 330 BP; 76 A; 89 C; 83 G; 82 T; 0 other;

QY 996 ACTACATGAAGGCCAACATTGCTGTCTGGACAGAGCCAGCAGTCAGTGTGAAAGTTGCTTGGA 1055

Db 330 ACTACATGAAGGCCAACATTGCTGTCTGGACAGAGCCAGCAGTCAGTGTGAAAGTTGCTTGGA 271

QY 1056 CATGCAAGGSGCATGCCTTCTACACACTAGAGCCCTCATCCACACAGACTAGTGCCTGCACT 1115

Db 270 CATGGCAAGGGCATGCCTTCTACACACTAGAGCCCTCATCCACACAGACTAGTGCCTGCACT 211

QY 1116 CAATACCGCTGTGTATGATGATGAGGAGATGACTGCCCCAATTAGCTTGGCTGATGT 1175

Db 210 CAATAGCCGTGTGTATGATGATGAGGAGATGACTGCCCCAATTAGCTTGGCTGATGT 151

QY 1176 CAAGTCTCTTCCAAATGCTCTGGTGCATGTATGACCTCTGGTAGGCCCGGAAGC 1235

Db 150 CAAGTCTCTTCCAAATGCTCTGGTGCATGTATGACCTCTGGTAGGCCCGGAAGC 91

QY 1236 TCTGCAAGAGGAGCTGAGACACAGACAGGCTCAGCACATGGAGTTTGCACT 1295

Db 90 TCTGCAAGAGGAGCTGAGACACAGACAGGCTCAGCACATGGAGTTTGCACT 31

QY 1296 GCTTCCTGTGGAACTGGTGAACGACGGGAGGT 1325

Db 30 GCTTCCTGTGGAACTGGTGAACGACGGGAGGT 1

RESULT 13
ABL16568
ID ABL16568 standard; DNA; 4354 BP.
XX ABL16568;
XX DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1177.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.

PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 1; Page 4235-4236; 980pp; English.
 XX
 CC AAH32943 to AAH3198 and AAH3514 to AAH7788 represent human colon
 cancer-associated nucleic acid molecules (N) and proteins (P), where
 the proteins are collectively known as colon cancer antigens. The colon
 therapy and vaccine production. N and P may be used in the prevention,
 diagnosis and treatment of diseases associated with inappropriate P
 expression. For example, N and P may be used to treat disorders
 associated with decreased expression by rectifying mutations or deletions
 in a patient's genome that affect the activity of P by expressing
 inactive proteins or to supplement the patients own production of P.
 Additionally, N may be used to produce the colon cancer-associated Ps,
 by inserting the nucleic acids into a host cell and culturing the cell,
 to express the proteins. N and P can be used in the prevention, diagnosis
 and treatment of colorectal carcinomas and cancers. AAH3796 to AAH7204
 and AAH7789 represent sequences used in the exemplification of the
 present invention.

CC - Pages 666 to 682 and page 7053 of the sequence listing were
 missing at time of publication, meaning no sequences are present for
 SEQ ID No:1027 to 1052, 7921 and 7922.

XX Sequence 568 BP; 148 A; 136 C; 143 G; 129 T; 12 other;
 XX Query Match 13.5%; Score 240.8; DB 22; Length 568;
 Best Local Similarity 97.2%; Pred. No. 2.4e-57;
 Matches 245; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 451 CACGGGAATGTGCCCTGCACTATGCCGTGTTGGGCCAGATCAAGTGCGAGGAC 510
 Db 2 CACGGGAATGTGCCCTGCACTATGCCGTGTTGGGCCAGATCAAGTGCGAGGAC 61

QY 511 CTGGTGCAMATGGGCCCTGTGCACTGTGAAAGTGTGGAGAGATGCCCTGGAC 570
 Db 62 CTGGTGCAMATGGGCCCTGTGCACTGTGAAAGTGTGGAGAGATGCCCTGGAC 121

QY 571 AAAGCCAAGGACCCCTGAGAGAGCTCTGGAGAGAGAGATGGCAGAAT 630
 Db 122 AAAGCCAAGGACCCCTGAGAGAGCTCTGGAGAGAGATGGCAGAAT 181

QY 631 CTCAACCGTATTCATAACAGACATTCTGGAAAGGGACACCCGACTGGCCCCGA 690
 Db 182 CTCAACCGTATTCATAACAGACATTCTGGAAAGGGACACCCGACTGGCCCCGT 241

QY 691 ATGGGACCCCTG 702
 Db 242 GAGTCACCACIG 253

RESULT 15
 ABX74732/C
 ID ABX74732 standard; cDNA; 285 BP.
 AC
 AC ABX74732;
 DT 21-MAR-2003 (first entry)
 DE Human cDNA sequence #55 differentially expressed in CC-RCC types.
 XX Human; microarray; solid surface; immobilised probe; CC-RCC;
 KW differential expression profile; aggressive CC-RCC tumour type;
 KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
 KW gene expression profiling; tumour tissue; gene; ss.
 OS Homo sapiens.
 XX
 PN WO200279411-A2.
 XX
 PD 10-OCT-2002.
 XX
 PP 29-MAR-2002; 2002WO-US09576.

XX Search completed: September 22, 2003, 17:14:38
 DE Job time : 374 secs

XX 29-MAR-2001; 2001US-279411P.
 PR
 XX
 FA (VAND-) VAN ANDEL INST.
 XX
 PT Haab B, Rhodes D, Teh BT, Takashi M;
 XX DR
 XX
 WPI: 2003-040579/03.

XX Claim 1; SEQ ID NO 386; 179pp; English.

CC The present invention relates to a microarray comprising a matrix of
 CC probes from a set of probes immobilised to a solid
 CC surface in a predetermined order, where a row of pixels corresponds
 CC to replicates of one distinct probe from the set. The probes are
 CC complementary to nucleic acid sequences that are expressed
 CC differentially in aggressive as compared to non-aggressive types of
 CC clear cell renal carcinoma (CC-RCC) and that hybridise to the probes
 CC under high stringency conditions. The microarray is useful for the
 CC prognosis of patients with CC-RCC, wherein aggressive and
 CC non-aggressive CC-RCC tumour types are characterised by differential
 CC expression profiles of genes that hybridise with one or more probes
 CC immobilised on the microarray. The arrays are useful for gene
 CC expression profiling of tumour and normal tissues. The present
 CC sequence represents a human cDNA sequence differentially expressed
 CC in aggressive vs. non-aggressive type CC-RCC phenotypes.

XX Sequence 285 BP; 57 A; 72 C; 86 G; 66 T; 4 other;
 XX Query Match 12.8%; Score 228.8; DB 25; Length 285;
 Best Local Similarity 97.4%; Pred. No. 4.1e-54;
 Matches 263; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

QY 1513 TAGGACTGGAGGTCC-TTGCCTGAACTCCAGAGGTGTCGGACATGGTGGGAATGC 1571
 Db 270 TAGGACTGGAGGTCTTGTGCTGAACTCCAGAGGTGTCGGACATGGTGGGAATGC 211

QY 1572 ACCTCCCAAAGCAGCAGGCCCTCTGGTGCCTCCCGCCCTCACTCATGTACTACCCC 1631
 Db 2110 ACCTCCCAAAGCAGCAGGCCCTCTGGTGCCTCCCGCCNCAGGTATGTACTACCCC 151

QY 1632 AGCC-TGGGTCCATCCCTTCCCATCCCTACCACTGT-GGGAAAGGGGGGGCTC 1689
 Db 150 AGCC-TGGGTCCATCCCTTCCCATCCCTACCACTGT-GGGAAAGGGGGGGCTC 91

QY 1690 AGAGCTTGTCACTTGCCACATGGTGTCCCAAACATGGAGGGATGCCCGCGCTGTC 1749
 Db 90 AGAGCTTGTCACTTGCCACATGGTGTCCCAAACATGGAGGGATGCCCGCGCTGTC 31

QY 1750 ACAATAAGTTATTATGAAAAAAA 1779
 Db 30 ACAATAAGTTATTATGAAAAAAA 1

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 22, 2003, 17:02:09 ; Search time 96 Seconds
 (without alignments)
 8225.359 Million cell updates/sec

Title: US-09-840-704A-1
Perfect score: 1789
Sequence: 1 gattatctcgcgactgt.....aaaaaaaaaaaaaaa 1789
Scoring table: IDENTITY_NUC
Gappen: Gappp 10.0 , Gapext 1.0

Searched: 56978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 113956

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Maximum Match 0%
 Listing first 45 summaries

Post-processing: Minimum Match 0%
 Maximum Match 100%
 List first 45 summaries

Database :

- Issued_Patent_NA:*
- 1: /cgn2_6/prodata/2/ina/5A-COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/5B-COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A-COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B-COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/CTUS-COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1789	100.0	1789	3 US-09-035-706-1
2	1789	100.0	1789	3 US-08-055-841-1
3	1789	100.0	1789	4 US-09-90-425-1
4	1789	100.0	1789	4 US-09-966-905-1
5	1787.4	99.9	1789	4 US-09-228-219-3
6	1771.4	99.0	1786	4 US-09-016-434-1071
7	133.8	7.5	152	1 US-08-00-575-35
8	75.4	4.2	2894	4 US-09-020-312D-95
9	71.2	4.0	1288	2 US-09-172-977-2
10	61.6	3.4	486	4 US-09-102-705-1406
11	61.6	3.4	486	4 US-09-196-457-1406
12	61.6	3.4	4134	3 US-09-196-387-1
13	61.6	3.4	4134	4 US-09-941-835-1
14	61.6	3.4	4491	4 US-09-96-387-7
15	61.6	3.4	4491	4 US-09-941-835-7
16	61.6	3.4	4657	3 US-09-196-387-9
17	61.6	3.4	4657	4 US-09-41-835-9
18	58	3.2	3454	3 US-09-082-059-1
19	58	3.2	14770	4 US-09-220-132-30
20	56.2	3.1	1026	4 US-09-94-110A-3
21	56.2	3.1	1318	3 US-08-986-304-1
22	54.4	3.0	2505	4 US-09-158-457-9
23	54.4	3.0	3026	4 US-09-58-457-7
24	54.2	3.0	3234	1 US-08-264-534-31
25	54.2	3.0	3234	1 US-08-083-590A-10
26	54.2	3.0	3234	1 US-08-665-500-31
27	54.2	3.0	3234	2 US-08-346-128-31

ALIGNMENTS

RESULT 1	SEQUENCE 1, Application US/09035706	PARENT NO. 6001622	GENERAL INFORMATION:
APPLICANT: Deahar, Shoukat	APPLICANT: Hannigan, Greg		
TITLE OF INVENTION: Integrin-Linked Kinase an	TITLE OF INVENTION: Its Uses		
NUMBER OF SEQUENCES: 11	NUMBER OF SEQUENCES: 11		
CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:		
ADDRESSEE: Bozicevic & Reed, LLP	STREET: 285 Hamilton Avenue, Suite 200		
CITY: Palo Alto	CITY: Palo Alto		
STATE: CA	STATE: CA		
ZIP: 94301	ZIP: 94301		
COUNTRY: USA	COUNTRY: USA		
COMPUTER READABLE FORM:	COMPUTER READABLE FORM:		
OPERATING SYSTEM: DOS	OPERATING SYSTEM: DOS		
SOFTWARE: FASTSEQ FOR Windows Version 2.0	SOFTWARE: FASTSEQ FOR Windows Version 2.0		
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/09/035,706	APPLICATION NUMBER: US/09/035,706		
FILING DATE:	FILING DATE:		
CLASSIFICATION:	CLASSIFICATION:		
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:		
APPLICATION NUMBER: 3	APPLICATION NUMBER: 3		
FILING DATE:	FILING DATE:		
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:		
NAME: Sherwood, Pamela J.	NAME: Sherwood, Pamela J.		
REGISTRATION NUMBER: 36,677	REGISTRATION NUMBER: 36,677		
REFERENCE/DOCKET NUMBER: KIN-2C1P1	REFERENCE/DOCKET NUMBER: KIN-2C1P1		
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:		
TELEPHONE: 650-327-3400	TELEPHONE: 650-327-3400		
TELEFAX: 650 327-3231	TELEFAX: 650 327-3231		
TELEFAX:	TELEFAX:		
INFORMATION FOR SEQ ID NO: 1:	INFORMATION FOR SEQ ID NO: 1:		
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:		
LENGTH: 1789 base pairs	LENGTH: 1789 base pairs		
TYPE: nucleic acid	TYPE: nucleic acid		
STRANDEDNESS: double	STRANDEDNESS: double		
TOPOLOGY: linear	TOPOLOGY: linear		
MOLECULE TYPE: cDNA	MOLECULE TYPE: cDNA		
US-09-035-706-1	US-09-035-706-1		
Query Match	100.0%; Score 1789; DB		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1789; Conservative 0; Mismatches	0;		

Sequence 10, Appl
Sequence 31, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 14809, A
Sequence 403, App
Sequence 1, Appl
Sequence 257, App
Sequence 257, App
Sequence 3, Appl
Sequence 1, Appl
Sequence 31, Appl
Sequence 1, Appl

Qy 1 GAATTCACTGTGACTCTGCTTACCAACGGAGTTCCCGGAGAGGATTCCTGCAGGCCAGT 60
 Db 1 GAAATTCACTGTGACTCTGCTTACCAACGGAGTTCCCGGAGAGGATTCCTGCAGGCCAGT 60
 Qy 61 CCCGAGGATAAAGCTGGTTCATCTCCCTTCCCTGATACTCCACAGCCTCAGGT 120
 Db 61 CCCGAGGATAAAGCTGGTTCATCTCCCTTCCCTGATACTCCACAGCCTCAGGT 120
 Qy 121 TCCCCAATCCAGGGACTCTGCGCCGGAGGCTGCTATGGACGACATTTCACAGTCG 180
 Db 121 TCCCCAATCCAGGGACTCTGCGCCGGAGGCTGCTATGGACGACATTTCACAGTCG 180
 Qy 181 CGGGAGGGCAGCAGTGCCTTCGCTTGCTGGACACACCGAGAACCTCAAC 240
 Db 181 CGGGAGGGCAGCAGTGCCTTCGCTTGCTGGACACACCGAGAACCTCAAC 240
 Qy 241 CAGGGGGAGATCATGGCTTCCTCCCTGACTGGCGCTCTGCT 300
 Db 241 CAGGGGGAGATCATGGCTTCCTCCCTGACTGGCGCTCTGCT 300
 Qy 301 GTGGGTGAGATGTTGATCATGGGGCACGGATCAATGTAATGAAACCTGGGATGAC 360
 Db 301 GTGGGTGAGATGTTGATCATGGGGCACGGATCAATGTAATGAAACCTGGGATGAC 360
 Qy 361 ACCCCCCCTGCATCTGCAGCCAGTATGACACCCTGATATTGACAGAACGCTATGCG 420
 Db 361 ACCCCCCCTGCATCTGCAGCCAGTATGACACCCTGATATTGACAGAACGCTATGCG 420
 Qy 421 TACAAGGGAGACATCAATGAGTGAATGGCCGGAGGATTAATGTAATGAACTGGGATGAC 480
 Db 421 TACAAGGGAGACATCAATGAGTGAATGGCCGGAGGATTAATGAACTGGGATGAC 480
 Qy 481 TTTTGGGCCAGAGATGAGTGGAGGACCTGGCCGAAATGGGGCCCTTGTAGCATC 540
 Db 481 TTTTGGGCCAGAGATGAGTGGAGGACCTGGCCGAAATGGGGCCCTTGTAGCATC 540
 Qy 541 TGTAACAGATATGGAGAGATGCCCTGGACAAGGGACCCCTGAGAGGCTTC 600
 Db 541 TGTAACAGATATGGAGAGATGCCCTGGACAAGGGACCCCTGAGAGGCTTC 600
 Qy 601 CGAGAGGGGAGGACCCGCACTGGGCCGAAATGGGACCTGGCTGAACACTTC 660
 Db 601 CGAGAGGGGAGGACCCGCACTGGGCCGAAATGGGACCTGGCTGAACACTTC 660
 Qy 661 TGGAAAGGGACCCGCACTGGGCCGAAATGGGACCTGGCTGAACACTTC 720
 Db 661 TGGAAAGGGACCCGCACTGGGCCGAAATGGGACCTGGCTGAACACTTC 720
 Qy 721 GACTTCAAACAGCTTAACTCTGACGAAAGCTCACTCTGGAGAGCTATGG 780
 Db 721 GACTTCAAACAGCTTAACTCTGACGAAAGCTCACTCTGGAGAGCTATGG 780
 Qy 781 AAGGGCCGCTGGCAGGGCAATGACATTGCTGAAAGCTGCTGAGACTGGGT 840
 Db 781 AAGGGCCGCTGGCAGGGCAATGACATTGCTGAAAGCTGCTGAGACTGGGT 840
 Qy 841 ACAAGGGAGAGGAGGACCTCAATGAGAGTGTCCCCTGCTCAGGATTTCGATCCA 900
 Db 841 ACAAGGGAGAGGAGGACCTCAATGAGAGTGTCCCCTGCTCAGGATTTCGATCCA 900
 Qy 901 AATGTCGTCCTCCAGTGTGGCTCCACCTGACAGTGTCTCATCCFACTCTCATC 960
 Db 901 AATGTCGTCCTCCAGTGTGGCTCCACCTGACAGTGTCTCATCCFACTCTCATC 960
 Qy 961 ACACACTGATGCCGATGGATCTACATGTCATGAAAGCCACAAATTGCTC 1020
 Db 961 ACACACTGATGCCGATGGATCTACATGTCATGAAAGCCACAAATTGCTC 1020
 Qy 1021 GTGGACCAAGGCAGGCTGAGGTTGCTGGAGATGGCAAGGGCATGCCCTCA 1080
 Db 1021 GTGGACCAAGGCAGGCTGAGGTTGCTGGAGATGGCAAGGGCATGCCCTCA 1080
 Qy 1081 CACACACTAGGCCCTCATCCACGACATGCACTCAATGCCCTGATGTTGAT 1140

Db 1081 CACACACTAGGCCCTCATCCACGACATGCACTCAATGCCCTGATGTTGAT 1140
 Qy 1141 GAGGACATGACTGCTGGGAATTAGCPTGGTGTGATGTCAGTCTCTTCCAAATGCGTACTCAATGCCCTGATGTTGAT 1200
 Db 1141 GAGGACATGACTGCTGGGAATTAGCPTGGTGTGATGTCAGTCTCTTCCAAATGCGTACTCAATGCCCTGATGTTGAT 1200
 Qy 1201 CGCATGTCATGCCCTGGTGTGAGCTGCCGAAGCTGAAAGGCCACA 1260
 Db 1201 CGCATGTCATGCCCTGGTGTGAGCTGCCGAAGCTGAAAGGCCACA 1260
 Qy 1261 AACAGACGCTCAGCAGACATGTCAGCTCCATGCTGGAAACTCTGGTGCACGG 1320
 Db 1261 AACAGACGCTCAGCAGACATGTCAGCTCCATGCTGGAAACTCTGGTGCACGG 1320
 Qy 1321 GAGGPACCCCTTGTGACTCTCCATATGGAGTTGGATGAAGCTGCGATTGGAGGC 1380
 Db 1321 GAGGPACCCCTTGTGACTCTCCATATGGAGTTGGATGAAGCTGCGATTGGAGGC 1380
 Qy 1381 CTTCGGCCCTAACATCCACAGGTATTCCCTCATGTTGTAACCTCATGAAATGCTGC 1440
 Db 1381 CTTCGGCCCTAACATCCACAGGTATTCCCTCATGTTGTAACCTCATGAAATGCTGC 1440
 Qy 1441 ATGAAAGAACGACCCCTGCAAGCACCACATTGACATGATTGCTGCTATCCTTGAGAAG 1500
 Db 1441 ATGAAAGAACGACCCCTGCAAGCACCACATTGACATGATTGCTGCTATCCTTGAGAAG 1500
 Qy 1501 ATGCCAGGACAGTAGCTGAGCTGAAAGCTCTGCTTAACTCAGAGTGTGGGAATGGT 1560
 Db 1501 ATGCCAGGACAGTAGCTGAGCTGAAAGCTCTGCTTAACTCAGAGTGTGGGAATGGT 1560
 Qy 1561 TGGGGAAATGACCTCCAAAGGAGCAGGCTCAGGCTCAGGCTCCGGCTCCAGTCAT 1620
 Db 1561 TGGGGAAATGACCTCCAAAGGAGCAGGCTCAGGCTCAGGCTCCGGCTCCAGTCAT 1620
 Qy 1621 GGTACTACCCAGCTGGCTTGTGACTTCCTCCATCCCTACACTGTGCGCAAGAGG 1680
 Db 1621 GGTACTACCCAGCTGGCTTGTGACTTCCTCCATCCCTACACTGTGCGCAAGAGG 1680
 Qy 1681 GGCGSCTCTGAGGCTTGTGACTTCCTCCATCCCTACACTGTGCGCAAGAGG 1740
 Db 1681 GGCGSCTCTGAGGCTTGTGACTTCCTCCATCCCTACACTGTGCGCAAGAGG 1740
 Qy 1741 CGCGCTGTCACATAAAAGTTTATGAAAMAAAAAAA 1789
 Db 1741 CGCGCTGTCACATAAAAGTTTATGAAAMAAAAAAA 1789

RESULT 2
 US-09-955-841-1
 ; Sequence 1, Application US/08955841
 ; Patent No. 6013782
 ; GENERAL INFORMATION:
 ; APPLICANT: Debarat, Shoukat
 ; APPLICANT: Hannigan, Greg
 ; TITLE OF INVENTION: Integrin-Linked Kinase and
 ; TITLE OF INVENTION: its Uses
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: Bozicevic & Reed, LLP
 ; STREET: 285 Hamilton Avenue, Suite 200
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ FOR Windows Version 2.0
 ; APPLICATION NUMBER: US/08/955,841
 ; FILING DATE:

CLASSIFICATION: 800
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sherwood, Pamela J
 REGISTRATION NUMBER: 36,677
 REFERENCE/DOCKET NUMBER: KIN-2C1P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-327-3400
 TELEX:
 TELEFAX: 650 327-3231
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1789 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-955-841-1

QY	721 GACTCAAAAGCTTAACCTCTGACGAAGCTCAACGAGAATCACTCTGGAGAGCTATGG
Db	721 GACTCAAAAGCTTAACCTCTGACGAAGCTCAACGAGAATCACTCTGGAGAGCTATGG
Qy	781 AASGCCSCTGGCAGGCAATGACATTGTCAGGTCCTGAAGGTTGAGACTGGAT
Db	781 AASGCCSCTGGCAGGCAATGACATTGTCAGGTCCTGAAGGTTGAGACTGGAT
Qy	840 AGGGCCGCGTGCAGGCCATGACATTGTCAGGTCCTGAAGGTTGAGACTGGAT
Db	840 AGGGCCGCGTGCAGGCCATGACATTGTCAGGTCCTGAAGGTTGAGACTGGAT
Qy	841 ACAGGAGAGCAGGGACTCACTGAGAGTGTCCCGCTCAGGTTTTCGATCCA
Db	841 ACAGGAGAGCAGGGACTCACTGAGAGTGTCCCGCTCAGGTTTTCGATCCA
Qy	900 .901 ATATGTCCTCCAGTGTCTAGTGTGCCAGTCTCACCTGCTCCATCTACTCTCATC
Db	900 .901 ATATGTCCTCCAGTGTCTAGTGTGCCAGTCTCACCTGCTCCATCTACTCTCATC
Qy	960 961 ACACACTGGATGCCGATGATGATCCTCTCAATGACTACTATGAGGCCAACATTGTC
Db	961 ACACACTGGATGCCGATGATGATCCTCTCAATGACTACTATGAGGCCAACATTGTC
Qy	961 ACACACTGGATGCCGATGATGATCCTCTCAATGACTACTATGAGGCCAACATTGTC
Db	961 ACACACTGGATGCCGATGATGATCCTCTCAATGACTACTATGAGGCCAACATTGTC

RESULT 3

US-09-390-425-1

Sequence 1, Application US/09390425

Patent No. 6338958

GENERAL INFORMATION:

APPLICANT: Dedha, Shoukat

APPLICANT: Hannigan, Greg

TITLE OF INVENTION: Integrin-Linked Kinase and its Uses

FILE REFERENCE: KIN-2CON

CURRENT APPLICATION NUMBER: US/09/390,425

CURRENT FILING DATE: 1999-09-03

EARLIER APPLICATION NUMBER: US6/0009,074

EARLIER FILING DATE: 1995-12-21

EARLIER APPLICATION NUMBER: US88/752,345

EARLIER FILING DATE: 1996-11-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 1

LENGTH: 1789

TYPE: DNA

ORGANISM: H. sapiens

FEATURE: CDS

NAME/KEY: CDS

LOCATION: (157) . . . (1512)

NAME/KEY: Other

LOCATION: (0) . . . (0)

US-09-390-425-1

	Query	Match	Score	Length
	QY	1 GAATTCACTGTCGACTGTACCAAGGGAGTTCCCGGAGAAAGGATC	1789	DB 4 ; Length 0 ; Indels 0
	Db	1 GAATTCACTGTCGACTGTACCAAGGGAGTTCCCGGAGAAAGGATC	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	61 CCCGAGGATAAAGCTTGGGTTCATCTCCCTTGATGACTCCTA	100.0%	Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	61 CCCGAGGATAAAGCTTGGGTTCATCTCCCTTGATGACTCCTA	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	121 TCCCCAAATCCAGGGAACTTCGCCGGGCCGGGAGCGCTGTATGGACGATC	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	121 TCCCCAAATCCAGGGAACTTCGCCGGGCCGGGAGCGCTGTATGGACGATC	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	181 CGGGAGGGCAAACGCACTCGCCGTTGGCCTGTGGCTGGACACACGGAA	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	181 CGGGAGGGCAAACGCACTCGCCGTTGGCCTGTGGCTGGACACACGGAA	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	241 CAGGGGGACGATCATGGCTTCCCTTGCACITGGCTGGCAGAA	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	241 CAGGGGGACGATCATGGCTTCCCTTGCACITGGCTGGCAGAA	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	301 GTGGTTGAGATGTTGATCATGGGGGGGACGGGATCAATGTAATGAA	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	301 GTGGTTGAGATGTTGATCATGGGGGGGACGGGATCAATGTAATGAA	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	361 ACCCCCCCTGCAATCTGGCAAGCCAGTCATGGCACCCGTATTTGTCACAA	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	361 ACCCCCCCTGCAATCTGGCAAGCCAGTCATGGCACCCGTATTTGTCACAA	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	421 TACAAGGAGACATCAATGGCAAGATCACTGGCAAGGACCTGATGTCACAA	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	421 TACAAGGAGACATCAATGGCAAGGACCTGATGTCACAA	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	481 TTCTTGGGCCAAGATACTGGCAAGATGTCAGGACCTGATGTCACAA	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	481 TTCTTGGGCCAAGATACTGGCAAGATGTCAGGACCTGATGTCACAA	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	541 TGTAACTAACATATGGAGATGCGCTGTGGACAAAAGCCAAGGCCCT	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Db	541 TGTAACTAACATATGGAGATGCGCTGTGGACAAAAGCCAAGGCCCT	100.0%	Best Local Similarity 100.0% ; Pred. No. 0 ; Mismatches 0 ;
	Qy	601 CGAGAGGGGGAGAGAGAGATGGCCAGAGATGGGAAATCTAACCGTATTCATA	100.0%	Matches 1789 ; Conservative 100.0% ; Pred. No. 0 ; Mismatches 0 ;

Db	601	CGAGGGCCAGAAAGATGGCCAGAATCTAACCGTATTCCATACAGGACATTC	660
Qy	661	TGAAAGGGACCAACCGACTCGCCGAATGGAACTCTGCATT	720
Db	661	TGAAAGGGACCAACCGACTCGCCGAATGGAACTCTGCATT	720
Qy	721	GACTTCAAACAGCTTAACCTCTTGAAAGGCTCAACGAAATCCTGGAGACTATGG	780
Db	721	GACTTCAAACAGCTTAACCTCTTGAAAGGCTCAACGAAATCCTGGAGACTATGG	780
Qy	781	AAGGCCCTGGAGGGAAATGACTGTGCGAAGGTGCTGAGGTTGAGCTGGAGT	840
Db	781	AAGGCCCTGGAGGGAAATGACTGTGCGAAGGTGCTGAGGTTGAGCTGGAGT	840
Qy	841	ACAAGGAGAGGAGGAGGAGCTTAACTGAAGAGTGTCCCCGGCTCAGGATTTCCTCCATCCA	900
Db	841	ACAAGGAGAGGAGGAGCTTAACTGAAGAGTGTCCCCGGCTCAGGATTTCCTCCATCCA	900
Qy	901	AATGTCCTCCAGTGTGAGGTGCTGCGAAGTCTCACCTGCTCTCATCCTACTCTCATC	960
Db	901	AATGTCCTCCAGTGTGAGGTGCTGCGAAGTCTCACCTGCTCTCATCCTACTCTCATC	960
Qy	961	ACACACTGATGCGTAGGGATCCCTTACAATGTACTACATGAGGACCAATTTCCTGTC	1020
Db	961	ACACACTGATGCGTAGGGATCCCTTACAATGTACTACATGAGGACCAATTTCCTGTC	1020
Qy	1021	GTGACCAGAGCCAGGTGTGAAGTTCTCTGGACATGGCAAGGGCATGGCTTCCTA	1080
Db	1021	GTGACCAGAGCCAGGTGTGAAGTTCTCTGGACATGGCAAGGGATGGCTTCCTA	1080
Qy	1081	CACACACTGAGGCCCTCATCCCAGACATGCACTCAATAGCGTAGCTGTAATGATTGAT	1140
Db	1081	CACACACTGAGGCCCTCATCCCAGACATGCACTCAATAGCGTAGCTGTAATGATTGAT	1140
Qy	1141	GAGGACATGACTGCCGATTAGCATGGCTGATGTCAAGTTCTCAATGCTCTGGT	1200
Db	1141	GAGGACATGACTGCCGATTAGCATGGCTGATGTCAAGTTCTCAATGCTCTGGT	1200
Qy	1201	CGCATGATGACCTGCCGGTAGCCCCGAAAGCTCTCGAGAAAAGCCTGAAAGACACA	1260
Db	1201	CGCATGATGACCTGCCGGTAGCCCCGAAAGCTCTCGAGAAAAGCCTGAAAGACACA	1260
Qy	1261	AACAGACCTCAGAGCATGCGATTGTTGCGAGTCTGCGAAGCTGGTCAACCG	1320
Db	1261	AACAGACCTCAGAGCATGCGATTGTTGCGAGTCTGCGAAGCTGGTCAACCG	1320
Qy	1321	GAGTACCCCTTGCTGACCTCTCCATAATGGAGATGGATGAAATGAGGTGAAATGAG	1380
Db	1321	GAGTACCCCTTGCTGACCTCTCCATAATGGAGATGGATGAAATGAGGTGAAATGAG	1380
Qy	1381	CTTCGGCTTACCATCCTACCGGTTTCCCTCATGTTGAAAGCTCATGAAAGTCTG	1440
Db	1381	CTTCGGCTTACCATCCTACCGGTTTCCCTCATGTTGAAAGCTCATGAAAGTCTG	1440
Qy	1441	ATGAATGAGACCTGCAAGGACCCAATTTGACATGATGTTGCTPATCCTGAGAAG	1500
Db	1441	ATGAATGAGACCTGCAAGGACCCAATTTGACATGATGTTGCTPATCCTGAGAAG	1500
Qy	1501	ATCGGAAAGTGTGACCTGGGACTGGAGGTCTTCCTGAACTTCAGGTTGCTGGAGCATGGT	1560
Db	1501	ATCGGAAAGTGTGACCTGGGACTGGAGGTCTTCCTGAACTTCAGGTTGCTGGAGCATGGT	1560
Qy	1561	TGGGGATGTGACCTGGGCTGATCCCTTCCCACATCCCTAACACTGTGCAAGAGG	1680
Db	1561	TGGGGATGTGACCTGGGCTGATCCCTTCCCACATCCCTAACACTGTGCAAGAGG	1680
Qy	1621	GGTACTACCCAGCTGGGTCTGAGGTGCACTGGTCCATCCCCCTCCAGTCAT	1740
Db	1621	GGTACTACCCAGCTGGGTCTGAGGTGCACTGGTCCATCCCCCTCCAGTCAT	1740
Qy	1681	GGGGGGTCAAGTGGGACTGGGCTCTGGGTTCTCCCAAAAGCAAGGGCCCTCTCCAGTCAT	1740

Db 1681 GCGGGGCTCAGAGCTTGTCACTGCCACATGGAGGGATCAGCC 1740
 Qy 1741 CGCCCTGTCAAGATAAAGTTATTATGAMAAAAAAA 1789
 Db 1741 CGGCCTGTCAAGATAAAGTTATTATGAAAAAAAAAAA 1789

RESULT 4
 US-09-566-906-1
 ; Sequence 1, Application US/09566906
 ; Patent No. 6369205
 ; GENERAL INFORMATION:
 ; APPLICANT: Dedhar, Shoukat
 ; TITLE OF INVENTION: Integrin-linked Kinase and its Uses
 ; FILE REFERENCE: KIN-2CON
 ; CURRENT APPLICATION NUMBER: US/09/566, 906
 ; CURRENT FILING DATE: 2000-05-09
 ; PRIOR APPLICATION NUMBER: 09/390, 425
 ; PRIOR FILING DATE: 1999-09-03
 ; PRIOR APPLICATION NUMBER: US08/752, 345
 ; PRIOR FILING DATE: 1996-11-19
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 1789
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (157)...(1512)
 ; LOCATION: (0)...(0)
 ; US-09-566-906-1

Query Match 100.0%; Score 1789; DB 4; Length 1789;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1789; Conservative 0;

Qy 1 GAAATCACCTGCTGACTGCTAACACGGGAGTCGGAGGATCTGGAGCCGAGT 60
 Db 1 GAATTCATCTCTGCTGACTCTCCCTCTCCCTGATCTACTCCACAGGGACT 60
 Qy 61 CCCGAGGATAAGCTTGGGTCATCTCTCTCCCTGATCTACTCCACAGGGACT 60
 Db 61 CCCGAGGATAAGCTTGGGTCATCTCTCTCCCTGATCTACTCCACAGGGACT 120
 Qy 121 TCCCCATCCGGGACTCTGGCGCCGGACCTCTGATGGAGGACATTTCCTACTAGTG 180
 Db 121 TCCCCATCCGGGACTCTGGCGCCGGACCTCTGATGGAGGACATTTCCTACTAGTG 180
 Qy 181 OGGGAGGGCAAGGAGCTCGCGGTGCGCTGTCGACACACGGAGAAGACCTAAC 240
 Db 181 OGGGAGGGCAAGGAGCTCGCGGTGCGCTGTCGACACACGGAGAAGACCTAAC 240
 Qy 241 CAGGGGAGCAGTCATGCTCTCCCTTGACTGGCCTCCGAGAGGGCGCTCTGCT 300
 Db 241 CAGGGGAGCAGTCATGCTCTCCCTTGACTGGCCTCCGAGAGGGCGCTCTGCT 300
 Qy 301 GTGGTGTAGAGTGTGATCATGGAGGACGGATCAATGTAATGACCTTGGGATGAC 360
 Db 301 GTGGTGTAGAGTGTGATCATGGAGGACGGATCAATGTAATGACCTTGGGATGAC 360
 Qy 361 ACCCCCCTGCTCTGGAGCAGCTGGAGACGGTATGTACAGAAAGCTATTGCA 420
 Db 361 ACCCCCCTGCTCTGGAGCAGCTGGAGACGGTATGTACAGAAAGCTATTGCA 420
 Qy 421 TACAAGGCAGACATCATGCTGAACAGGGATGTCAGGATCTGGCA 480
 Db 421 TACAAGGCAGACATCATGCTGAACAGGGATGTCAGGATCTGGCA 480
 Qy 481 TTGGGGCCAGATGCGAGGGACTGGCAATGGGCCCTTGTCACT 540
 Db 481 TTGGGGCCAGATGCGAGGGACTGGCAATGGGCCCTTGTCACT 540
 Qy 541 TGTACAGATGAGGAGATGCCCTGCAAGAACCAAGCACCTGAGAGGCTTC 600
 Db 541 TGTACAGATGAGGAGATGCCCTGCAAGAACCAAGCACCTGAGAGGCTTC 600
 Qy 601 CGAGACGGGAGAGAATCTCACCGATTCCTCAAGAACACATT 660
 Db 601 CGAGACGGGAGAGAATCTCACCGATTCCTCAAGAACACATT 660
 Qy 661 TGGAGGGGACCCGACTCGGCCCGIAATGAACTGAAACACACTCTGCATT 720
 Db 661 TGGAGGGGACCCGACTCGGCCCGIAATGAACTGAAACACACTCTGCATT 720
 Qy 721 GACTCAACAGCTRACTCTGAGAAGCTAACGGAGATCACTCTGGAGCTATGG 780
 Db 721 GACTCAACAGCTRACTCTGAGAAGCTAACGGAGATCACTCTGGAGCTATGG 780
 Qy 841 ACAAGAGAGAGGAGCTCAATORAGACTGTCGGGCTCAGGATTCTCGATCCA 900
 Db 841 ACAAGAGAGAGGAGCTCAATORAGACTGTCGGGCTCAGGATTCTCGATCCA 900
 Qy 901 AATGTCCTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 960
 Db 901 AATGTCCTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 960
 Qy 961 ACACACTGGATGCCCTATGGATCCCTCTACATGACTACATGAGGACCAATTGTC 1020
 Db 961 ACACACTGGATGCCCTATGGATCCCTCTACATGACTACATGAGGACCAATTGTC 1020
 Qy 1021 GTGGACAGAGCCAGCTGTAAGTGTGAGGTTGCTTGGCATGCAASGGGATGGCTCTCA 1080
 Db 1021 GTGGACAGAGCCAGCTGTAAGTGTGAGGTTGCTTGGCATGCAASGGGATGGCTCTCA 1080
 Qy 1081 CACACCTAGAGCCCTCATCCACAGCATGCACTCATGGCGTAGTGAATGATTGAT 1140
 Db 1081 CACACACTAGAGCCCTCATCCACAGCATGCACTCATGGCGTAGTGAATGATTGAT 1140
 Qy 1141 GAGGAGATGACTGCCCTCATCCACAGCATGCACTCATGGCGTAGTGAATGATTGAT 1200
 Db 1141 GAGGAGATGACTGCCCTCATCCACAGCATGCACTCATGGCGTAGTGAATGATTGAT 1200
 Qy 1201 CGCAGTATGACCTGGCTGGTAGCCCCGAAAGCTCTGAGAAGAAAGCTGAAGACACA 1260
 Db 1201 CGCAGTATGACCTGGCTGGTAGCCCCGAAAGCTCTGAGAAGAAAGCTGAAGACACA 1260
 Qy 1261 AACAGAGCTCAGGAGACATGGAGTTGCACTGGCTCTGTGGAGCTGGACAGACCG 1320
 Db 1261 AACAGAGCTCAGGAGACATGGAGTTGCACTGGCTCTGTGGAGCTGGACAGACCG 1320
 Qy 1320 AACAGAGCTCAGGAGACATGGAGTTGCACTGGCTCTGTGGAGCTGGACAGACCG 1320
 Db 1320 AACAGAGCTCAGGAGACATGGAGTTGCACTGGCTCTGTGGAGCTGGACAGACCG 1320
 Qy 1380 GAGGACCTTGTGCACTCCAAATGGAGATGGTAAGGTTGGGATGGCA 1380
 Db 1380 GAGGACCTTGTGCACTCCAAATGGAGATGGTAAGGTTGGGATGGCA 1380
 Qy 1381 CTTCGCTTACCATCCACAGGTATTTCCTCTATGGAGATGGTAAGGTTGGGATGGCA 1440
 Db 1381 CTTCGCTTACCATCCACAGGTATTTCCTCTATGGAGATGGCA 1440
 Qy 1440 ATGAGTGAACCCCTGCAAGGCCAAATTGACATGATGTTGCACTGAGATCTG 1500
 Db 1440 ATGAGTGAACCCCTGCAAGGCCAAATTGACATGATGTTGCACTGAGATCTG 1500
 Qy 1501 ATGAGGACAAGTAGCTGAAGGATGTCCTGCACTGCCCTGAGAG 1560
 Db 1501 ATGAGGACAAGTAGCTGAAGGATGTCCTGCACTGCCCTGAGAG 1560
 Qy 1560 TGGGGAGATCACCTCCAAAGGAGGAGGATGGCAATGGGCCCTTGTCACT 1620
 Db 1560 TGGGGAGATCACCTCCAAAGGAGGAGGATGGCAATGGGCCCTTGTCACT 1620

Qy	1621	GCTACTACCCAGCCTGGTCCATCCCCCTCCCATCCCCATCCCTACCACTGTCGCCAAAGAGG 1680	Db	481	TTTGGGCCAAGATCAAGTGGCAGAGGACTGGGCCAAATGGGCCCTGTGTCAGCATC 540
Db	1621	GCTACTACCCAGCCTGGTCCATCCCCATCCCTACCACTGTCGCCAAAGAGG 1680	Qy	541	TGTAACAACATPATGGAGAGATGCCCTGTCGACAAAGCCAAAGGCCACCCCTGAGAGAGCTTC 600
Qy	1681	GCGGGCTCAGAGCTTGTCACTTGCCACATGGTCTCCAAACATGGGAGGGATCAGCC 1740	Db	541	TGTAACAAGATGGAGATGCCCTGTCGACAAAGCCAAAGGCCACCCCTGAGAGCTTC 600
Db	1681	GCGGGCTCAGAGCTTGTCACTTGCCACATGGTCTCCAAACATGGGAGGGATCAGCC 1740	Qy	601	CGAGGCGGGAGAAAGATGGCAGAAATCTCAAGGPAATTCCATACAGGACACATT 660
Qy	1741	CGGCCGTGACATAAAGTTTATTATGAAAAAAA 1789	Db	601	CGAGGCGGGAGAAAGATGGCAGAAATCTCAAGGPAATTCCATACAGGACACATT 660
Db	1741	CGGCCGTGACATAAAGTTTATTATGAAAAAAA 1789	Qy	661	TGGAACGGGACCCGCACTGGCCCAAATGGAAACCTGTGACAAACACTCTGCATT 720
Db	1741	CGGCCGTGACATAAAGTTTATTATGAAAAAAA 1789	Db	661	TGGAACGGGACCCGCACTGGCCCAAATGGAAACCTGTGACAAACACTCTGCATT 720
RESULT 5					
US-09-428-219-3 Application US/09428219					
Sequence No. 6177273					
GENERAL INFORMATION:					
APPLICANT: C. Frank Bennett					
APPLICANT: Lex M. Cowser					
TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION					
FILE REFERENCE: RTS-0101					
CURRENT APPLICATION NUMBER: US/09/428, 219					
CURRENT FILING DATE: 1999-10-27					
NUMBER OF SEQ ID NOS: 89					
SEQ ID NO: 3					
LENGTH: 1789					
TYPE: DNA					
ORGANISM: Homo sapiens					
FEATURE:					
NAME/KEY: CDS					
LOCATION: (157) .. (1515)					
US-09-428-219-3					
Query Match 99.9%; Score 1787.4; DB 3; Length 1789;					
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;					
Matches 1788; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	1	GAATTATCTGCACTGCTACCACGGAGTTCCCGGAGAGGATCCTGGAGCCAGT 60	Db	1081	CACACACTAGAGGCCCTCATCCCACGACATGCAATTGCTGAAATGGATTGAT 1140
Db	1	GAATTATCTGCACTGCTACCACGGAGTTCCCGGAGAGGATCCTGGAGCCAGT 60	Qy	1081	CACACACTAGAGGCCCTCATCCCACGACATGCAATTGCTGAAATGGATTGAT 1140
Qy	61	CCCGAGGATAAAAGCTTGGGTCATCCCTCCPTCCCTGAACTCCACGTCCTAGGCT 120	Db	1141	GAGGACATGACTGCCGAATTAGCTGGCTGATGTCGAAGTTCTTCCAATGTCCTGGT 1200
Db	61	CCCGAGGATAAAAGCTTGGGTCATCCCTCCPTCCCTGAACTCCACGTCCTAGGCT 120	Qy	1141	GAGGACATGACTGCCGAATTAGCTGGCTGATGTCGAAGTTCTTCCAATGTCCTGGT 1200
Qy	121	TCCCCAATCCACGGGACTCGGGCTGCTATGGGACATTTCACTCTGTC 180	Db	1201	CGCATGATGACCTGGCTGATGTCGAAGTTCTTCCAATGTCCTGGT 1260
Db	121	TCCCCAATCCACGGGACTCGGGCTGCTATGGGACATTTCACTCTGTC 180	Qy	1201	CGCATGATGACCTGGCTGATGTCGAAGTTCTTCCAATGTCCTGGT 1260
Qy	181	CGGGAGGCAAGCAGCTGCCGTTGCCGAGCGGACCTCAAC 240	Db	1261	AACAGACGCTCAGCACACATGGGAACTTGTGGAACTTGTGCAAGCAGG 1320
Db	181	CGGGAGGCAAGCAGCTGCCGTTGCCGAGCGGACCTCAAC 240	Qy	1261	AACAGACGCTCAGCACACATGGGAACTTGTGGAACTTGTGCAAGCAGG 1320
Qy	241	CAGGGAGGATCATGGCTTCTCCCTGTGACTGGCTCCGAGGGCCGCTGT 300	Db	1321	GAGGTACCCCTTGCACCCCTCCAAATGGGAACTGGGAACTTGTGCAAGCAGG 1380
Db	241	CAGGGAGGATCATGGCTTCTCCCTGTGACTGGCTCCGAGGGCCGCTGT 300	Qy	1321	GAGGTACCCCTTGCACCCCTCCAAATGGGAACTGGGAACTTGTGCAAGCAGG 1380
Qy	301	GTGGTGTGAGCTGTGATGACATGGTAAATGTAACCGTGGGATGAC 360	Db	1381	CTTCGGCCCTACATCCCGTCAAAAGCGACCCCTCAATCTGCTTGAAG 1440
Db	301	GTGGTGTGAGCTGTGATGACATGGTAAATGTAACCGTGGGATGAC 360	Qy	1381	CTTCGGCCCTACATCCCGTCAAAAGCGACCCCTCAATCTGCTTGAAG 1440
Qy	361	ACCCCTCTGCACTGCGAGCTGGCTGTCGCTGACACGGAAACCTCAAC 420	Db	1441	ATGAATGAAAGCCCTCAAAAGCGACCCCTCAATCTGCTTGAAG 1500
Db	361	ACCCCTCTGCACTGCGAGCTGGCTGTCGCTGACACGGAAACCTCAAC 420	Qy	1441	ATGAATGAAAGCCCTCAAAAGCGACCCCTCAATCTGCTTGAAG 1500
Qy	421	TACAAGCCAGACATCAATGGCAGTGAATGAAACCGGAATGTCGCTGT 480	Db	1501	ATGCAGGACAGTGAACCTGGCTGTCGCTGACCTGTCGCTGAAATGG 1560
Db	421	TACAAGCCAGACATCAATGGCAGTGAATGAAACCGGAATGTCGCTGT 480	Qy	1501	ATGCAGGACAGTGAACCTGGCTGTCGCTGACCTGTCGCTGAAATGG 1560
Qy	481	TTTGGGGCCAAAGATCAATGGCAGAGGACCTGGCTGTCGCTGAAATGG 540	Db	1561	TGGGGAAATGCACCCCTCCCAAAAGCAGCAGGGCTCCTCCGCTCCAGTCAT 1620
Qy	481	TTTGGGGCCAAAGATCAATGGCAGAGGACCTGGCTGTCGCTGAAATGG 540	Db	1561	TGGGGAAATGCACCCCTCCCAAAAGCAGCAGGGCTCCTCCGCTCCAGTCAT 1620

RESULT 7
 US-08-700-575-35
 ; GENERAL INFORMATION:
 ; Sequence 35 Application US/08700575
 ; Pat. No. 5817479
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hawkins, Phillip R.
 ; APPLICANT: Wilde, Craig G.
 ; TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08/700,575
 ; APPLICATION NUMBER: US/08/700,575
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BILLINGS, LUCY J
 ; REGISTRATION NUMBER: 36749
 ; REFERENCE/DOCKET NUMBER: SP-100 US
 ; TELECOMMUNICATION INFORMATION:

RESULT 8
 US-09-620-312D-95
 ; GENERAL INFORMATION:
 ; Sequence 95 Application US/09620312D
 ; Pat. No. 6569662
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Ma, Yunqiang
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: John Tillinghast
 ; APPLICANT: Drmanac, Radmila T.
 ; TITLE OF INVENTION: Nucleic Acids and
 ; POLYPEPTIDES
 ; FILE REFERENCE: 784CIPB
 ; CURRENT APPLICATION NUMBER: US/09/620,312D
 ; CURRENT FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 1105
 ; SOFTWARE: pc_FL_genes Version 1.0
 ; SEQ ID NO 95
 ; LENGTH: 2894
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (372) .. (2894)
 ; US-09-620-312D-95

Qy 1201 CGCATGTATGCCCTGGTAGCCCCAAGCTCTGAGAACAGCTGGAGACACA 1260
 Db 1201 CGCATGTATGCCCTGGTAGCCCCAAGCTCTGAGAACAGCTGGAGACACA 1260
 Qy 1261 AACAGAGCTCAGCACATGGAACTTGGACTTTCAGTCCTCTGTGACACGG 1320
 Db 1261 AACAGAGCTCAGCACATGGAACTTGGACTTTCAGTCCTCTGTGACACGG 1320
 Qy 1321 GAGGTACCTTGTGACCTCCAAATGGAGATGGAAATGAAAGTGATTGGAAAGGC 1380
 Db 1321 GAGGTACCTTGTGACCTCCAAATGGAGATGGAAAGTGATTGGAAAGGC 1380
 Qy 1381 CTTCGGCTTACATCCCCACCAAGGTATTCCCTCATGGTGTAACTCAAGAGTCGC 1440
 Db 1381 CTTCGGCTTACATCCCCACCAAGGTATTCCCTCATGGTGTAACTCAAGAGTCGC 1437
 Qy 1441 ATGAATGAAAGACCCCTGAAACGCCAAATTGACATGATTGGCTATCCTTGAAAG 1500
 Db 1438 ATGAATGAAAGACCCCTGAAACGCCAAATTGACATGATTGGCTATCCTTGAAAG 1497
 Qy 1501 ATGCGGACAAAGTAGGACTGAAAGTCCTGCTGAACTCCAGAGTCGGGAGATGCT 1560
 Db 1498 ATGCGGACAAAGTAGGACTGAAAGTCCTGCTGAACTCCAGAGTCGGGAGATGCT 1557
 Qy 1561 TGGGGAAATGAACTCCAAAGCACGGCTCTGGTTGCTCCCCGCTCCAGTCAT 1620
 Db 1558 TGGGGAAATGAACTCCAAAGCACGGCTCTGGTTGCTCCCCGCTCCAGTCAT 1617
 Qy 1621 GTTACTACCCAGGCTGGGTCAATCCCCTCCACACTGTGCCAAAGGG 1680
 Db 1618 GTTACTACCCAGGCTGGGTCAATCCCCTCCACACTGTGCCAAAGGG 1677
 Qy 1681 GCGGGGTCAAGCTTGTCACTTGCCACATGGTGTCTCCAAACATGGAGGGATGCC 1740
 Db 1678 GCGGGGTCAAGCTTGTCACTTGCCACATGGTGTCTCCAAACATGGAGGGATGCC 1737
 Qy 1741 CGGGCTGTCAATAAGTTATTATGAAAAA..... 1789
 Db 1738 CGGGCTGTCAATAAGTTATTATGAAAAA..... 1786
 RESULT 7
 US-08-700-575-35
 ; GENERAL INFORMATION:
 ; Sequence 35 Application US/08700575
 ; Pat. No. 5817479
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hawkins, Phillip R.
 ; APPLICANT: Wilde, Craig G.
 ; TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08/700,575
 ; APPLICATION NUMBER: US/08/700,575
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BILLINGS, LUCY J
 ; REGISTRATION NUMBER: 36749
 ; REFERENCE/DOCKET NUMBER: SP-100 US
 ; TELECOMMUNICATION INFORMATION:

Query Match 4.2%; Score 75.4; DB 4; Length 2894;
 Best Local Similarity 52.4%; Pred. No. 2.2e-11; Matches 166; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

Qy 269 TCCACTGGGCCCTGCCAGAGGCGCCCTGTGCTGGTGTGACATGTGCAATTGCGGG 328
 Db 439 TOCACTGGCCAGCATCATGGCCACTTGGAATGGTGTAGCATTCATGGCGGG 498
 Qy 329 CACGGATCAAGTAATGAAACGGTGGGATGACACCCCTGCATCTGGCACCCAGCATG 388
 Db 499 CAGAAGTGACTCTGAAGGATAAGAGAACAGGTTATACCCCTCTCATGTCAGCAGCTCCAATG 558

Qy 389 GACACCCTGATATGTCAGAGCTATGCACTACAGGACATCAATCCAGTGATG 448
 Db 559 GACAGATTAATGTTGTCAGATCTCTGAAACCTGGGGAGATGTGAATCAATG 618

Qy 449 AACACGGAAATACAGCCTTCACATGCCCTGACTATGCCCTTGGGCCAGATCAAGTGGCGAGG 508
 Db 619 TCTATGAAATACAGCCTTCACATGCCCTGACTATGCCCTTGGGCCAGATCAAGTGGCGAGG 678

Qy 509 ACCTGCTGGCAATGGGCCCTTGTCAAGCACTGTACAGTACATGAGATGGCTGTG 568
 Db 679 AGTTGATTGACTACGGTGTCAAGTGTGAAACCAACAATATGGTTCAACCCCTTGC 738

Qy 569 ACAAGCCAAGGCACCC 585
 Db 739 ATTTCGTGCTCC 755

RESULT 9
 US-09-172-977-2
 ; Sequence 2, Application US/09172977
 ; Patent No. 5989863
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Corley, Neill C.
 ; APPLICANT: Yue, Henry
 ; TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
 ; FILE REFERENCE: PF-0615 US
 ; CURRENT APPLICATION NUMBER: US/09/172,977
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PPerl Program
 ; SEQ ID NO: 2
 ; LENGTH: 1288
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: -
 ; OTHER INFORMATION: 1808075
 ; US-09-172-977-2

Query Match 4.0%; Score 71.2; DB 2; Length 1288;
 Best Local Similarity 48.3%; Pred. No. 2.3e-10; Matches 199; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

Qy 226 GAGAACGACCTCAACCAAGGGGAGCATCAGCTCTCCCTTCACTGGCCCTGCCA 285
 Db 690 GACAACACTCGTCACAGACGCCAGACGCCGCGCTCACCCCTCATCTGGCCCTGCC 749

Qy 286 GAGGGCGCTCTGCTGGTGTAGATGTGATCATGGGGGACGGATCAATGTAATG 345
 Db 750 TTGGAGAGATGTGAGCTGGGACGGTGTGCTCTGAGTGGGTGCGACCCACATCTG 809

Qy 346 AACCGTGGGATGACACCCCCCTGCACTGCGACGGCAGGTCAATGAAACCGTGTATGT 405
 Db 810 GCAAAGAGGCGAGAGGCGCTGTGCTGCCAGCACGGCGCTAACAGAACATG 869

Qy 406 AGAAAGCTATTCAGTACAAGCAGACATCATGCGATGAAACAGGCGATGCGC 465
 Db 870 GGGCTGCTGCTGGAGCATCATATGATGGAAATGGAGGGAGGCCA 929

Qy 466 CTGCACTATGCCTGTTGGGCCAGATCAAGTGGCAGAGGACCTGGTGGCAATGGG 525

RESULT 10
 US-09-702-705-1406
 ; Sequence 1405, Application US/09702705
 ; Patent No. 6504010
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A..
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C14
 ; CURRENT FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 1833
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 1406
 ; LENGTH: 486
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-702-705-1406

Query Match 3.4%; Score 61.6; DB 4; Length 486;
 Best Local Similarity 49.7%; Pred. No. 7.5e-08; Matches 157; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

Qy 254 ATGGCTTCTCCCTCTGACTGGGCTGCGAGGGCCCTCTGTGTGTGAGATG 313
 Db 166 ATGGCTGACTCCCTACATTATGGAGCTCTGCAAAAACAGGCATGTGATGCTGTCATG 225

Qy 314 TGATCATGGGGGACGGATCAATGTAATGAAACGGTGGGATGACACCCCCCTGCTC 373
 Db 226 TACTGGAGGGGGCTTAATCCAGATGCTAGGACATTATGAGGGCTCATGAC 285

Qy 374 TGGCAGCAGTCATGGCACCGTGATATGAGGATATGGAGTACATCTCTGACTACAACTCA 433
 Db 286 GGCGAGGAGCAAGGGTAATGGAGATGTTGATTCATCTCTGACTACAACTCA 345

Qy 434 TCAATGAGATGAAACGGGATGTGCCCTGCATATGCGCTTGTGGGCCAG 493
 Db 346 CAACATTCAGACACTGAGGGTACATCTCTGACTACATAGCTGTTGAGGAGAG 405

Qy 494 ATCAAGTGGAGAGGACTCTGGGCAATGGGCCTGTCAGCATCTGAAACAGTATG 553
 Db 406 TGGAAAGAGCAAACCTGCTGGTGTGCCAGAGGACAGTATACATGGAAATAGAG 465

Qy 554 GAGAGATGCTGTGGA 569
 Db 466 AAAAGACACCCCTGCA 481

RESULT 11
 US-09-736-457-1406
 ; Sequence 1406, Application US/09736457
 ; Patent No. 6509448
 ; GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Lodes, Michael A.
 APPLICANT: Fanger, Gary
 APPLICANT: Vednick, Tom
 APPLICANT: Carter, Darrick
 APPLICANT: Retter, Marc
 APPLICANT: Mannion, Jane
 APPLICANT: Fan, Liqun
 APPLICANT: Wang, Ajun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121.47C15
 CURRENT APPLICATION NUMBER: US/09/736,457
 CURRENT FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 1864
 SEQ ID NO: 1406
 LENGTH: 486
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-736-457-1406

Query Match 3 4%; Score 61.6; DB 4; Length 486;
 Best Local Similarity 49.7%; Pred. No. 7.5e-08;
 Matches 157; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

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Qy 254 ATGGCTTCCTCCCTTGCACTGGCTTGCCGAGGGCGCTGCTGTGGTGGATGT 313
Db 166 ATGGCTCATCTCCCTPACATTATGAGCTTGAAAAAACGCCATAGATGGCTGTGATGT 225
Qy 314 TGATCATGGGGGGGACGGATCAATGTAATGAAACGGGGATACACCCCTGCAATC 373
Db 226 TACTGGAGGGGGGTTAATCGATGCTAACAGGACCATATGAGGCTAACAGTGCACC 285
Qy 374 TGGCAGCCAGTCATGGCACCCGTGATATTGACAGAGCTATTGGCTAACAGGAGACA 433
Db 286 GGGCAGAGCCAAAGGGTAACITGAAGATGATCATTCCTCTGAAAGCATCCA 345
Qy 434 TCAATGCGTAGTGAATGAAACCGGAATGCCCCCTGGACTATGCCMGTGTTGGGCCAAG 493
Db 346 CAAACATCAAGAACACTGGGGTAACACTCTCTACACTTAGCCCTGTGAGGAGAG 405
Qy 494 ATCAAATGGCAGGAGGACCTGGTGGCAATAATGGGCCCTTGTGAGCATCTGTAACAGATG 553
Db 406 TGGAAAAGCAAAACGTGGTGGTCCCAGGGAGAATAGAGAAG 465
Qy 554 GAGAGATGCCCTGGAA 569
Db 466 AAAAGAACCCCTGCA 481

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Query Match 3 4%; Score 61.6; DB 3; Length 4134;
 Best Local Similarity 51.1%; Pred. No. 2.3e-07;
 Matches 145; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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Qy 189 CAACCGCAGTGCGCTTCGCGCTGCGCTGCGACAAACZCGGAGAACGACTAACCCGGGGA 248
Db 2087 CAACCGCAGTGCGCTTCGCGCTGCGACAAACZCGGAGAACGACTAACCCGGGGA 2146
Qy 249 CGATATGGCTTCCTCCCTGCAATGGCTGGCCCTGCGAGAGGGCCCTGCTGTGTTGA 308
Db 2147 CAAGGGTGGCTGGCCCTCTCATATGGACACTATGGCATATGGCTGTCAATGGCTGTGA 2206
Qy 309 GATTTGATCATGGGGGGACGGATCAATGTAATGAAACCGTGGGATGACACCCCT 368
Db 2207 GCTTTAGTAGGGATGGGCTTCTGTCAATGTGGGAATTATCCCTCT 2266
Qy 369 GCATCTGGCAGCCAGTCATGGACACCGTATATGTCAGAAAGCTATTGGAGTACAGGC 428
Db 2267 CCATGAAGGAGCAGTAAAGGAAAGTGAATCTGCAACCTCTTAAACATGGAC 2326
Qy 429 AGACATCAATGCGTAGTGAATGAAACAGGGAAATGTGCCCTGCACT 472
Db 2327 AGATCCCACTAAAAAGAACAGAGATGGAATAACACTTGTGATT 2370

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RESULT 13
 US-09-841-835-1
 Sequence 1, Application US/09841835
 Patent No. 6506587

GENERAL INFORMATION:
 APPLICANT: de Lange, Titia
 APPLICANT: Smith, Susan
 TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
 TITLE OF INVENTION: OF USE THEREOF
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue, 4th Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/841,835

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 09/196,387

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-230 CIP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4134 base pairs

STRANDEDNESS: double

TYPE: nucleic acid

TOPOLogy: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

US-09-841-835-1

Query Match 3.4%; Score 61.6; DB 4; Length 4134;

Best Local Similarity 51.1%; Pred. No. 2.3e-07; Matches 145; Conservative 0; MisMatches 139; Indels 0; Gaps 0;

Qy 189 CAACCGCAGTCGCCGTTGGCAACACGGAGAACGCTCACCAAGGTCCGATGTCATGCCAAAGA 248

Db 2087 CAACCCGGTGTGTGTGTAGTACTGTCTACACCAGGTCCGATGTCATGCCAAAGA 2146

Qy 249 CGATCATGGCTCTCCCCCTGCACCTGGCCAGAGGGCCCTCTGGTGTGTGA 308

Db 2147 CAAGGGTGCTTGGCCCTCTCATATGCTGTGTCATAGGACACTATGGTGTGTGA 2205

Qy 309 GATGTTGATCATGGCTGGGGTCTGTCAARTGTGGGGACTATGGAAATTACCCCT 368

Db 2207 CCTTTTAGTAAGCATGGGTTCTGTCAARTGTGGGGACTATGGAAATTACCCCT 2266

Qy 369 GCATCTGGACCCAGCATGGATGGGATTCAGAGGATATTGCGTGTAGGC 428

Db 2267 CCATGAGCAGCAGCTAAAGGAATGAAATCTCAAGSTCTTTAAACATGGAGC 2326

Qy 429 AGACATCAATCAGTGATGACACGGGAATGTGCCCTGACT 472

Db 2327 AGATCCAACTAAGAAGACAGAGATGAAATACACCTTGATT 2370

RESULT 14

US-09-196-387-7

Sequence 7, Application US/09196387

; Patent No. 6227613

GENERAL INFORMATION:

APPLICANT: de Lange, Titia

TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

TITLE OF INVENTION: OF USE THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

Query Match 3.4%; Score 61.6; DB 3; Length 4491;

Best Local Similarity 51.1%; Pred. No. 2.4e-07; Matches 145; Conservative 0; MisMatches 139; Indels 0; Gaps 0;

Qy 189 CAACCGCAGTCGCCGTTGGCAACACGGAGAACGCTCACCAAGGTCCGATGTCATGCCAAAGA 248

Db 244 CAACCGGTTGTGTGTAGTACTGTCTACACCAGGTCCGATGTCATGCCAAAGA 2503

Qy 249 CGATGTGATCATGGCTGGGGACGGATCAATGTAATGAACTGGGATGACACTATGGTGTGTGA 308

Db 2504 CAAGGGTGCTTGGCCCTCTCATATGCTGTCTATGACACTATGGTGTGTGA 2563

Qy 309 GATGTTGATCATGGCTGGGGACGGATCAATGTAATGAACTGGGATGACACCCCCCT 368

Db 2564 GCTTTAGTAGGCTGGGGTCTGTCAATGTCGAGCTATGAAATTACCCCT 2623

Qy 369 GCATCTGGACCCAGCATGGATGGGATTCAGAGGATATTGCGTGTAGGC 428

Db 2624 CCATGAGCAGCAGCTAAAGGAATGAAATCTCAAGCTCCCTTTAAACATGGAGC 2683

Qy 429 AGACATCAATCAGTGATGACACGGGAATGTGCCCTGACT 472

Db 2684 AGATCCAACTAAGAAGACAGAGATGAAATACACCTTGATT 2727

RESULT 15

US-09-841-835-7

Sequence 7, Application US/09841835

; Patent No. 6506587

GENERAL INFORMATION:

APPLICANT: de Lange, Titia

TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

TITLE OF INVENTION: OF USE THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/841,835
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/196,387
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-477-5800
 TELEFAX: 201-343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4491 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 6..2027
 US-09-841-835-7

Query Match Score 3.4%; Score 61.6; DB 4;
 Best Local Similarity 51.1%; Pred. No. 2.4e-07;
 Matches 145; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
 Qy 189 CAACGGAGTCGCCGTTGCGCTGTGGCTGGACAAACGGAAACGACCTAACCGGGGA 248
 Db 2444 CAACCCGGTGTCTGTGAGTAGTACCTGCTAACACAGTGATGCCATGCCAAAAGA 2503
 Qy 249 CGATCATGCTCTCCTCCCTGCACTGGCTGCGCCAGGGCGCTCTGCTGTGGTGA 308
 Db 2504 CAAGGGTGGCTGGTCCCTCATATGCTGTCAATATGACACTATGAGTGGCTGA 2563
 Qy 309 GATGTTGATCATGGGGGGACGGATCAATGTAATGACACCCCT 368
 Db 2564 GCTTTAGTAAAGGATGGGTTCTCAATGTCGGGACTATGAAATTACCCCT 2623
 Qy 369 GCATCTGGCAGCCAGTCATGGACACGGTATTGAGTACAAGGC 428
 Db 2624 CCATGAGCAGGATAAGGAAAGTGAATCTCAAGTCCCTTAAACATGGAGC 2683
 Qy 429 AGACATCATGCGTGAATGACACCGGAATGCCCCGTGACT 472
 Db 2684 AGATCCAACTAAAAAGAACAGAGATGAAATACACCTTGATT 2727

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 Job time : 99 secs

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OM nucleic - nucleic search, using sw model

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(w/o alignment time)

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Minimum DB seq length: 0

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Maximum Match 100%
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Published Applications NA: *

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- 7: /cgn2_6/ptodata/2/pubpna/us08_PUBCOMB.seq: *
- 8: /cgn2_6/ptodata/2/pubpna/us09A_PUBCOMB.seq: *
- 9: /cgn2_6/ptodata/2/pubpna/us09B_PUBCOMB.seq: *
- 10: /cgn2_6/ptodata/2/pubpna/us09C_PUBCOMB.seq: *
- 11: /cgn2_6/ptodata/2/pubpna/us09_NEW_PUB.seq: *
- 12: /cgn2_6/ptodata/2/pubpna/us10A_PUBCOMB.seq: *
- 13: /cgn2_6/ptodata/2/pubpna/us10B_PUBCOMB.seq: *
- 14: /cgn2_6/ptodata/2/pubpna/us10_NEW_PUB.seq: *
- 15: /cgn2_6/ptodata/2/pubpna/us60_NEW_PUB.seq: *
- 16: /cgn2_6/ptodata/2/pubpna/us60_PUBCOMB.seq: *
- 17: /cgn2_6/ptodata/2/pubpna/us60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1789	100.0	1789	10 US-09-840-704-1
2	1352.6	75.6	1607	9 US-09-922-302-336
3	610	34.1	1013	12 US-09-814-353-20253
4	437.4	24.4	484	11 US-09-918-995-15193
5	427.6	23.9	464	11 US-09-918-995-23944
6	328.4	18.4	330	9 US-09-833-263-435
7	328.4	18.4	330	10 US-09-833-263-435
8	328.4	18.4	330	13 US-10-025-380-435
9	240.8	13.5	568	14 US-10-166-698-42638
10	170.2	9.5	506	12 US-09-814-353-14739
11	127.8	7.1	301	10 US-09-917-800A-187
12	123.2	6.9	462	12 US-09-814-353-14739
13	123.2	6.9	462	12 US-09-814-353-8355
14	85.9	5.0	197	10 US-09-733-590-22528
15	85.6	4.8	370	11 US-09-918-995-8469
16	75.6	4.2	2355	14 US-10-164-080-6

ALIGNMENTS

RESULT 1

Sequence 1, Application US/09940704

Patent No. US20020122801A1

GENERAL INFORMATION:

APPLICANT: Dedhat, Shoukat

APPLICANT: Harnigan, Greg

TITLE OF INVENTION: Integrgrin-Linked Kinase and its Uses

FILE REFERENCE: KIN-2CON

CURRENT APPLICATION NUMBER: US/09/840,704

CURRENT FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: 09/566,906

PRIOR FILING DATE: 2000-05-09

PRIOR APPLICATION NUMBER: US8/752,345

PRIOR FILING DATE: 1996-11-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1789

TYPE: DNA

ORGANISM: H. sapiens

FEATURE: CDS

NAME/KEY: CDS

LOCATION: (157)...(1512)

NAME/KEY: Other

LOCATION: (0)...(0)

US-09-840-704-1

Query Match Score 1789; DB 10; length 1789;
Best Local Similarity 100.0%; PRed. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1789; Conservative 0; Sequence 1789, A

QY 1 GAATTCACTGTGCGACTGTCACGCCGGAGTCCCGGAGAGAGATCTGCAGCCCCGAGT

1 GAATTCACTGTGCGACTGTCACGCCGGAGTCCCGGAGAGAGATCTGCAGCCCCGAGT

Db 1 GAATTCACTGTGCGACTGTCACGCCGGAGTCCCGGAGAGAGATCTGCAGCCCCGAGT

Db 1 CCCAGGAAATACCTTGGGGTCACTCCCTGGATCACTCCACGTTCTCGAGT

QY 61 CCCAGGAAATACCTTGGGGTCACTCCCTGGATCACTCCACGTTCTCGAGT

61 CCCAGGAAATACCTTGGGGTCACTCCCTGGATCACTCCACGTTCTCGAGT

61 CCCAGGAAATACCTTGGGGTCACTCCCTGGATCACTCCACGTTCTCGAGT

Qy	121	TCCCCAATCCAGGGACTCGGCCGAGCGACCTGGCTGCTATGGACGACATTTCACTCAGTGC	180	Qy	1201	CGCATGTATGCACCTGCCTGGTAGCCCCGAAGCTCTGAGAAAGAACAGCTGAAACACA	1260
Db	121	TCCCCAATCCAGGGACTCGGCCGAGCGACCTGGCTGCTATGGACGACATTTCACTCAGTGC	180	Db	1201	CGCATGTATGCACCTGCCTGGTAGCCCCGAAGCTCTGAGAAAGAACAGCTGAAACACA	1260
Qy	181	CGGAGGGCAACGGCAGTCGGCGTTCCCTGGCTGGACAAACACGGAGAACCTCAAC	240	Qy	1261	AACAGACGGCTCAGGAGACATGGGAGTTTGCACTGGCAACTCTGTCATGGAAAGCTGACGG	1320
Db	181	CGGAGGGCAACGGCAGTCGGCGTTCCCTGGCTGGACAAACACGGAGAACCTCAAC	240	Db	1261	AACAGACGGCTCAGGAGACATGGGAGTTTGCACTGGCAACTCTGTCATGGAAAGCTGACGG	1320
Qy	241	CAGGGGAGGATCATGGTCTCCCTGGACTGGGCTCTGGAGGGCGCTGTGCT	300	Qy	1321	GAGGTAACCCCTTGCTGACCCCTCCAAATATGGAGATGGGATGGTGGGAAAGGG	1380
Db	241	CAGGGGAGGATCATGGTCTCCCTGGACTGGGCTCTGGAGGGCGCTGTGCT	300	Db	1321	GAGGTAACCCCTTGCTGACCCCTCCAAATATGGAGATGGGATGGTGGGAAAGGG	1380
Qy	301	GTGGTGTGAGATGGTGTGATCACTGGGAGCCGGATAATGTAATGAAACCGGGATGAC	360	Qy	1381	CTTCGGCTTACCATCCACAGGTTTCCCTCTGTGTGTAAGCTCATGAAGTCTGC	1440
Db	301	GTGGTGTGAGATGGTGTGATCACTGGGAGGGATGAC	360	Db	1381	CTTCGGCTTACCATCCACAGGTTTCCCTCTGTGTGTAAGCTCATGAAGTCTGC	1440
Qy	361	ACCCCCCTGGCATCTGGCAGGACTGGGAGCCGGATAATGTAATGAAACGGCTATTGAG	420	Qy	1441	ATGATGAAAGACCCCTGCAAAAGGACCCAAATTGACATGATTGTCCTTGAAG	1500
Db	361	ACCCCCCTGGCATCTGGCAGGACTGGGAGGGATGAC	420	Db	1441	ATGATGAAAGACCCCTGCAAAAGGACCCAAATTGACATGATTGTCCTTGAAG	1500
Qy	421	TACAAGGAGGACATCATGGCTGATGTAACACGGGAATTGGCCCTGCACTATGGT	480	Qy	1501	ATGCAAGGACAAAGTAGGACTGGCTGCGCTTGGGGAGATGGTGGGAGATGGT	1560
Db	421	TACAAGGAGGACATCATGGCTGATGTAACACGGGAATTGGCCCTGCACTATGGT	480	Db	1501	ATGCAAGGACAAAGTAGGACTGGCTGCGCTTGGGGAGATGGTGGGAGATGGT	1560
Qy	481	TTTTGGGGCCAAGATACTGGTGGACAGGACTGGCCPTGTGACGATC	540	Qy	1561	TGGGGAAATGCACTCCCTCCCAAAGGCGCAGGGCTCTGGCTCCCGCCTCZGTCAT	1620
Db	481	TTTTGGGGCCAAGATACTGGTGGACAGGACTGGCCPTGTGACGATC	540	Db	1561	TGGGGAAATGCACTCCCTCCCAAAGGCGCAGGGCTCTGGCTCCCGCCTCZGTCAT	1620
Qy	541	TGTAACAAAGTATGGAGAGATGGCTGTGCAAGTGGACGGACCCCTGAGAGCTTC	600	Qy	1621	GGTACTAACCCCAGCTGGGTTGCACTCCCTACCCATCCCTACCAACTGTGCAAGAGG	1680
Db	541	TGTAACAAAGTATGGAGAGATGGCTGTGCAAGTGGACGGACCCCTGAGAGCTTC	600	Db	1621	GGTACTAACCCCAGCTGGGTTGCACTCCCTACCCATCCCTACCAACTGTGCAAGAGG	1680
Qy	601	CGAGAGGGGAGCACCCGACTGGCCAGAGATCTAACAGGACATTC	660	Qy	1681	GGGGGCTCTGAGCTTGTGACTCTGGGATCATGGGAGGGATCAGCC	1740
Db	601	CGAGAGGGGAGCACCCGACTGGCCAGAGATCTAACAGGACATTC	660	Db	1681	GGGGGCTCTGAGCTTGTGACTCTGGGATCATGGGAGGGATCAGCC	1740
Qy	661	TGAAAGGGGACCAACCGGACTCGGCCGACTGGCCGAAATGGAACACTCTGGCAT	720	Qy	1741	CGCGCTGTCAACATAAAAGTTTATGAAAAAAA	1789
Db	661	TGAAAGGGGACCAACCGGACTCGGCCGACTGGCCGAAATGGAACACTCTGGCAT	720	Db	1741	CGCGCTGTCAACATAAAAGTTTATGAAAAAAA	1789
Qy	721	GACTTCAACACGCTTAACCTCTGGAGGACTCACTCTGGAGGTATGG	780	RESULT			
Db	721	GACTTCAACACGCTTAACCTCTGGAGGACTCACTCTGGAGGTATGG	780	US-09-925-302-336			
Qy	781	AAGGGCGCTGGCAGGCGCAATGACATTGCTGTAAGCTGGACTCTGGAGT	840	; Sequence 336, Application US/0925302			
Db	781	AAGGGCGCTGGCAGGCGCAATGACATTGCTGTAAGCTGGACTCTGGAGT	840	; Patent No. US2004491A1			
Qy	841	ACAAGGAGGAGGGACATTCAATGAGAGTGTCCCGCTCAGATTCTGATCA	900	; GENERAL INFORMATION:			
Db	841	ACAAGGAGGAGGGACATTCAATGAGAGTGTCCCGCTCAGATTCTGATCA	900	; APPLICANT: Rosen et al.			
Qy	901	AATGTGCTCCAGTGTGGCTCAGTCTCAACCTGCTCATCTCATC	960	; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies			
Db	901	AATGTGCTCCAGTGTGGCTCAGTCTCAACCTGCTCATCTCATC	960	; FILE REFERENCE: PA104			
Qy	961	ACACACTGGATGCCGATGGCTCATGAGCTACATGAGCTACATGAGCTAC	1020	; CURRENT APPLICATION NUMBER: US/09/925,302			
Db	961	ACACACTGGATGCCGATGGCTCATGAGCTACATGAGCTACATGAGCTAC	1020	; PRIORITY APPLICATION NUMBER: PCT/US00/05918			
Qy	1021	GTGGACCAAGCCAGGCTGTAAGTTGCTTGGACATGGCAAGGGCATGGCTTCCTA	1080	; CURRENT FILING DATE: 2001-08-10			
Db	1021	GTGGACCAAGCCAGGCTGTAAGTTGCTTGGACATGGCAAGGGCATGGCTTCCTA	1080	; PRIORITY FILING DATE: 2000-03-08			
Qy	1081	CACACACTAGGCCCTCATCCACACATGACCTGCTCATCTCATC	1140	; PRIOR FILING DATE: 1999-03-12			
Db	1081	CACACACTAGGCCCTCATCCACACATGACCTGCTCATCTCATC	1140	; NUMBER OF SEQ ID NOS: 96			
Qy	1141	GAGGACATGACTGCCGAATTAGCATGGCTCCTTCATGTCATGGCTCTGGT	1200	; SOFTWARE: PatentIn Ver. 2.0			
Db	1141	GAGGACATGACTGCCGAATTAGCATGGCTCCTTCATGTCATGGCTCTGGT	1200	; SEQ ID NO: 336			
Qy				; LENGTH: 1607			
Db				; TYPE: DNA			
Qy				; ORGANISM: Homo sapiens			
Db				; FEATURE: misc feature			
Qy				; NAME/KEY: misc feature			
Db				; LOCATION: (1162)			
Qy				; OTHER INFORMATION: n equals a,t,g, or c			
Db				; NAME/KEY: misc feature			
Qy				; LOCATION: (1449)			
Db				; OTHER INFORMATION: n equals a,t,g, or c			
Qy				US-09-925-302-336			
Db				Query Match 75.6%; Score 1352.6;			
Qy				Best Local Similarity 99.5%; Pred. No. 0;			
Db				Matches 1375; Conservative 2; Indels 3; Gaps 2;			

QY 411 GCTATTCAGTACAAGSCAGACATCATGCACTGAATGAAACACGGAAATGTGCCCTGCA 470
Db 186 GCTATTGCACTGAGAACATCATGCACTGAATGAAACACGGAAATGTGCCCTGCA 245
QY 471 CTATGCCTTTTGSGCCIAAGATCAGATCAGTCAGTGAATGAAACACGGAAATGTGCCCTGCA 530
Db 246 CTATGCCTTTTGSGCCIAAGATCAGATCAGTCAGTGAATGAAACACGGAAATGTGCCCTGCA 305
QY 531 TGTCAAGCACTGTAACAGATGAGAGATGAGATGAGACCTGGTGGCAATTGGGCGCT 590
Db 306 TGTCAAGCACTGTAACAGATGAGAGATGAGATGAGACCTGGTGGCAATTGGGCGCT 365
QY 591 AGAGCTTCTCCAGAGSGGGAGAGAGATGGCCAGAATTCACCGTATCCATACAA 650
Db 366 AGAGCTTCTCCAGAGGGGGAGAGAGATGGCCAGAATTCACCGTATCCATACAA 425
QY 651 GGACACATTCTCGAAGGGGACACCGCACTGGCCGAAATGGACCCCTGAG 770
Db 426 GGACACATTCTCGAAGGGGACACCGCACTGGCCGAAATGGACCCCTGAG 485
QY 711 CTCGGGATTCAACTTCACACGCTTAACCTCTGAGAAGGAACTTCACCTCTG 770
Db 486 CTCGGGATTCAACTTCACACGCTTAACCTCTGAGAAGGAACTTCACCTCTG 545
QY 771 AGAGCTATGGAGGGCGCTGCGAGGCAATGACATGTCGAGGGTCTGAGGTTG 830
Db 546 AGAGCTATGGAGGGCGCTGCGAGGCAATGACATGTCGAGGGTCTGAGGTTG 605
QY 831 AGACTCTGAGTCAGAGAGACAGGGACTTCATGAGAGGTTCCGGCTCAGGTTT 890
Db 606 AGACTCTGAGTCAGAGAGACAGGGACTTCATGAGAGGTTCCGGCTCAGGTTT 665
QY 891 CTGGCATCCAATGTCCTCCAGTGTAGGCGCTGCGAGGTTCCGGCTCAGGTTT 950
Db 666 CTGGCATCCAATGTCCTCCAGTGTAGGCGCTGCGAGGTTCCGGCTCAGGTTT 725
QY 951 TACTCTCATCACACAGTGTAGGCGCTTACATGAGAGGTTCCGGCTCAGGTTT 1010
Db 726 TACTCTCATCACACAGTGTAGGCGCTTACATGAGAGGTTCCGGCTCAGGTTT 785
QY 1011 CAATTGTCCTGGGACAGACCGCTGAGTTGCTGGACATGCGAGGGCAT 1070
Db 786 CAATTGTCCTGGGACAGACCGCTGAGTTGCTGGACATGCGAGGGCAT 845
QY 1071 GCCTCTCTACACACACTAGGCCCCCTATCCACCGACATGCGAGTTGCTGGACATGCGAGGGCAT 1130
Db 846 GCCTCTCTACACACACTAGGCCCCCTATCCACCGACATGCGAGTTGCTGGACATGCGAGGGCAT 905
QY 1131 ATGATGATGATGAGGACATGATGTCGCGGATGATGCGATGTCAGTTCTTCA 1190
Db 906 ATGATGATGATGAGGACATGATGTCGCGGATGATGCGATGTCAGTTCTTCA 965
QY 1191 ATGTCCTGGTGTGATGACCTGCTGCTGCTGAGCTCTGCGAGGC 1250
Db 966 ATGTCCTGGTGTGATGACCTGCTGCTGAGCTCTGCGAGGC 1025
QY 1251 TGAGACACAACAGACGCTTGGAGACATGAGTTGAGGTTGCTGGAGCT 1310
Db 1026 TGAGACACAACAGACGCTTGGAGACATGAGTTGAGGTTGCTGGAGCT 1085
QY 1311 GGTGACACGGGAGGTACCTTGTGACCTCTCCAATATGAGGATGAGGTTGCTGGACAT 1370
Db 1086 GGTGACACGGGAGGTACCTTGTGACCTCTCCAATATGAGGATGAGGTTGCTGGACAT 1145
QY 1371 ATGGAGGGCCTCGGCTTACATCCACCGGATTCCTCATGTCAGTCAGTC 1430
Db 1146 ATGGAGGGCCTCGGCTTACATCCACCGGATTCCTCATGTCAGTCAGTC 1205
QY 1431 GAGATCTGCACTGAGACCTGCAAGGCAACATGAGATGAGGTTGCTGGACAT 1490
Db 1206 GAGATCTGCACTGAGACCTGCAAGGCAACATGAGATGAGGTTGCTGGACAT 1265

RESULT 3
US-09-814-353-20253
; Sequence 20253, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TREATMENT OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814, 353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191, 031
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/207, 124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211, 940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216, 820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220, 661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257, 672
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20253
; LENGTH: 1013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000,
; LOCATION: 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010,
; LOCATION: 1011, 1012, 1013
; OTHER INFORMATION: n = A,T,C or G

US-09-814-353-20253

Query Match 34 1%; Score 610; DB 12; Length 1013;
Best Local Similarity 98 %; Pred. No. 3e-181; 5; Indels 3; Gaps 2;
Matches 636; Conservative 0; Mismatches 1123 CGTAGCTGAATGATGATGAGGACATGACTGCCCAATTGACATGCTGAGTC 1182
Db 344 CGTCGGTAATGATGATGAGGACATGACTGCCCAATTGACATGCTGAGTC 403

Qy	1183	TCTTTCATAGTCCTGGTCCATGTATGACACTCTGGTAGCCCCAAGCTCTGGAG 1.24
Db	404	TCTTTCATGTCCTGGTCCATGTATGACACTCTGGTAGCCCCAAGCTCTGGAG 4.63
Qy	1243	AAGAGCCCTGAAGACACAAAGAGCTCAAGACACATGGGACTTGCAGACATGGGATTTGCACTGGAGTTTGAGCTCTGT 13.02
Db	464	AAAGAACCTGAAGACACAAAGAGCTCAAGACACATGGGACTTGCAGACATGGGAGTTTGAGCTCTGT 5.23
Qy	1303	TGGGAACACTGGTACACGGGGGTACCCCTTGTGACCTCTCCAAATATGGGAGATTGGAAATG 13.62
Db	524	TGGGAACACTGGTACACGGGGGTACCCCTTGTGACCTCTCCAAATATGGGAGATTGGAAATG 5.83
Qy	1363	AAGGTGGCATGGGGCCTTCGGGGCTACCCATCCACCGGATTTCCTCATGTGTGT 14.22
Db	584	AAGGTGGCATGGGGCCTTCGGGGCTACCCATCCACCGGATTTCCTCATGTGTGT 6.43
Qy	1423	AAGCTCATGAGATCTGGATGAATGAAAGAACGCCAAAGCAGCACAAATTGGACATGGATT 14.82
Db	644	AAGCTCATGAGATCTGGATGAATGAAAGAACGCCAAAGCAGCACAAATTGGACATGGATT 7.03
Qy	1483	GTGCCTATCCTTGAAGAGTGCAGGACAAGTAGGACTGGAAAGGTCTCTGGCTCTGAACCTCCA 15.42
Db	704	GTGCCTATCCTTGAAGAGTGCAGGACAAGTAGGACTGGAAAGGTCTCTGGCTCTGAACCTCCA 7.63
Qy	1543	GAGGTGGTGGGACATGGTGGGGAAATGACACTCCAAAAGCGAGGCGCTCTGGTGCC 1.602
Db	764	GAGGTGGTGGGACATGGTGGGGAAATGACACTCCAAAAGCGAGGCGCTCTGGTGCC 8.23
Qy	1603	TCCCCGGCTCCASTCATGCTACTACCCAGGCC-TGGGGTCCATCCTCTCCCCATCCC 16.61
Db	824	TCCCCGGCTCCAGCATGGTACTACCCAGGCC-TGGGGTCCATCCTCTCCCCATCCC 8.83
Qy	1662	TACCACTGTG-CGGAAGAGGGGGCTCAGACCTTGTCACTTGCACATGGTCTCT 17.19
Db	884	TACCACTGTGCCCCAAAGGGGGGGCTCAGACCTTGTCACTTGCACATGGTCTCT 9.43
Qy	1720	CCAAATGGGGGGTCAGGCCCCCTGTACACATAAAAGTTTAT 17.63
Db	944	CCAAATGGGGGGTCAGGCCCCCTGTACACATAAAAGTTTAT 9.87
RESULT 4		
US-09-918-995-15193		
Sequence 15193, Application US/09918995		
; Publication No. US0030073623A1		
; GENERAL INFORMATION:		
; APPLICANT: HYSEED, Inc.		
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED		
; FROM VARIOUS cDNA LIBRARIES		
; FILE REFERENCE: 20411-756		
; CURRENT APPLICATION NUMBER: US/09/918,995		
; PRIORITY FILING DATE: 2001-07-30		
; NUMBER OF SEQ ID NOS: 38054		
; SOFTWARE: FastSEQ For Windows Version 3.0		
; SEQ ID NO 15193		
; LENGTH: 484		
; TYPE: DNA		
; ORGANISM: Homo sapiens		
; FEATURE:		
; NAME/KEY: misc_feature		
; LOCATION: (1)..(484)		
; OTHER INFORMATION: n = A,T,C or G		
US-09-918-995-15193		
Query Match 24.4% Score 437.4; DB 11; Length 484;		
Best Local Similarity 99.5%; Pred. No. 4.9e-127;		
Matches 436; Conserv. 0; Mismatches 2; Indels 0; Gaps 0;		
; Qy 952 ACTCTCATCACACACTGGATGCCCTATGATCCCTACAATGTACTACATGAGGGACC 10.11		
; Db 44 ACCTCTCATCACACACTGGATGCCCTATGATCCCTACAATGTACTACATGAGGGACC 10.03		

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE: 210121_471C14
 CURRENT APPLICATION NUMBER: US/10/025,380
 CURRENT FILING DATE: 2001-12-19
 NUMBER OF SEQ ID NOS: 1129
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 435
 LENGTH: 330
 TYPE: DNA
 ORGANISM: Homo sapiens

Query Match 18.4%; Score 328.4; DB 113; Length 330;
 Best Local Similarity 99.7%; Pred. No. 8 8e-93; Indels 0; Gaps 0;
 Matches 329; Conservative 0; Mis matches 1; Name/KEY: misc feature
 LOCATION: (429) .(429)

Qy 996 ACTACATGAAAGCACCATAATTCTGTCTGGACAGAGCCAGGTGTGAAGTTGCTTGGAT 1055
 Db 330 ACTACATGAAAGCACCATAATTCTGTCTGGACAGAGCCAGGTGTGAAGTTGCTTGGAT 271
 Qy 1056 CATGGAAAGGGCATGGCTCTAACACACTAGGCCCTCATCCACACATGCACT 1115
 Db 270 CATGGAAAGGGCATGGCTCTAACACACTAGGCCCTCATCCACACATGCACT 211
 Qy 1116 CAAATGGCGTAACTGTAAATGATTGATGAGACATGCCGAATTAGCATGGCTGATGT 1175
 Db 210 CAATAGCGTGTGTTGATGATGATGAGACATGCCGAATTAGCATGGCTGATGT 151
 Qy 1176 CAAAGTCTCTTCCAAATGTCTGGTCGATCATGCACCTGGTAGCCCCGAAAGC 1235
 Db 150 CAAGTTCTTCCAAATGTCTGGTCGATCATGCACCTGGTAGCCCCGAAAGC 91
 Qy 1236 TCTGCGAAGAGGGCTTGAGACACAACAGACGCTCAGCAGACATGTGGAGTTTGCAGT 1295
 Db 90 TCTGCGAAGAGGGCTTGAGACACAACAGACGCTCAGCAGACATGTGGAGTTTGCAGT 31
 Qy 1296 GCTTCGTGGAACCTGTGACAGGGAGT 1325
 Db 30 GCTTCGTGGAACACTGGTACAGGGAGT 1
 RESULT 9
 US-10-106-698-2638
 ; Sequence 2638, Application US/10106698
 ; Publication No. US20030109630A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
 ; FILE REFERENCE: PA005P1
 ; CURRENT APPLICATION NUMBER: US/10/106,698
 ; PRIOR APPLICATION NUMBER: US 60/157,137
 ; PRIOR FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/26524
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: US 60/163,280
 ; NAME/KEY: misc feature
 ; LOCATION: (341) .(341)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (395) .(395)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (407) .(407)

OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (429) .(429)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (444) .(444)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (455) .(455)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (457) .(457)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (508) .(508)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (524) .(524)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (526) .(526)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (555) .(555)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (557) .(557)
 OTHER INFORMATION: n equals a,t,g, or c
 US-10-106-698-2638

Query Match 13.5%; Score 240.8; DB 14; Length 568;
 Best Local Similarity 97.2%; Pred. No. 4.6e-65;
 Matches 245; Conservative 0; Mis matches 7; Indels 0; Gaps 0;

Qy 451 CACGGAAATGTGCCCTGCACATATCCTGTTTGGCCAAGATCAAGTGGCAAGGGAC 510
 Db 2 CACGGAAATGTGCCCTGCACATATCCTGTTTGGCCAAGATCAAGTGGCAAGGGAC 61
 Qy 511 CTGGTGGCAAATGGGCCCTGAGAGAGCTCTGTACAAGTATGGAGAGATGCCCTGGGAC 570
 Db 62 CTGGTGGCAAATGGGCCCTGTCAGCATCTGTTTGGCCAAGATCAAGTGGCAAGGGAC 121
 Qy 571 AAAGGCAAAAGGCAACCCCTGAGAGAGCTCTGGAGAGATGGCAAGATGGCCAGAAT 630
 Db 122 AAAGGCAAAAGGCAACCCCTGAGAGAGCTCTGGAGAGATGGCAAGATGGCCAGAAT 181
 Qy 631 CTCAACCGTATTCCATACAGGACACATTCTGGAGGGACCCGACTCGGCCCGA 690
 Db 182 CTCAACCGTATTCCATACAGGACACATTCTGGAGGGACCCGACTCGGCCCGT 241
 Qy 691 AATGGAAACCCCTG 702
 Db 242 GAGTCACCACTG 253

RESULT 10
 US-09-814-353-14739
 ; Sequence 14739, Application US/0981453
 ; Publication No. US2003016531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, John
 ; APPLICANT: Thompson, Pamela
 ; APPLICANT: Lillie, James
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; THERAPY OF OVARIAN CANCER
 ; FILE REFERENCE: MRI-006B
 ; CURRENT APPLICATION NUMBER: US/09/814,353
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: US 60/191,031
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/207,124
 ; PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 60/211, 940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216, 820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220, 661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257, 672
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 14739
TYPE: DNA
ORGANISM: Homo sapiens
US-09-814-353-14739

Query Match 9.5%; Score 170.2; DB 12; Length 506;
Best Local Similarity 9.5%; Pred. No. 1.3e-29;
Matches 213; Conservative 0; Mismatches 82; Indels 6; Gaps 3;
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1123 CGTAGCTAATGATGAGACATGCCGAATTACATGCCTGATCTCAAGTC 1182
Db 332 CGTCCGGTAATGATGATGAGACATGCCTGCCGAATTACATGCCTGATCTCAAGTC 391

Qy 1183 TCTTCCAAATGCTCTGTCGATGTTGACTGCTGGTAGCCCGGAGCTCGAG 1242
Db 392 TCTTCCAAATGCTCTGTCGATGTTGACTGCTGGTAGCCCGGAGCTCGAG 451

Qy 1243 AGAAGCCTGAGACACAAGACGACCTCACAGACAGATGTTGAGTTTGAGTGC 1297
Db 452 AGAAGCCTGAGACACAAGACGACATGTTGAGTTTGAGTGC 506

RESULT 11
US-09-917-800A-187/c
Sequence 187, Application US/09917800A
Patent No. US20020119462A1

GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Blashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-503B-US

CURRENT APPLICATION NUMBER: US/09/917, 800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/290, 029
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222, 040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222, 880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290, 029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290, 645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292, 336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295, 798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297, 457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298, 884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303, 459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 187
LENGTH: 301
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE: misc_feature
LOCATION: 8
OTHER INFORMATION: n = A,T,C or G

US-09-917-800A-187
OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA866435
Query Match 7.1%; Score 127.8; DB 10; Length 301;
Best Local Similarity 7.0 8%; Pred. No. 1.3e-29;
Matches 213; Conservative 0; Mismatches 82; Indels 6; Gaps 3;
Matches 125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1493 TTGAGAGATGAGGAAAGTAGGTGGAGGTCCTSGCTGAACCTCAGAGGTCTGG 1552
Db 301 TCGAGAGATCAGACAGTAGGACTGAGTGTGGAGGTCCTGCCAAATTCAAGAGTATCAG 242

Qy 1553 GACATGGTTGGGGAGTCACTCCCAAAGCAGCAGGCCTCTGCTTGCCTCCCGCCT 1612
Db 241 CATATGCTGGACGATAAAATTCCCTGAAGTTGAGTTGAGTTGCTGCTGCCCTCGATGT 182

Qy 1613 CGAGTGTGACTACCCAG-CCTGGTCCATCCCCCTCCCATCTTACACTGT- 1670
Db 181 CTAATGCTGGACTACCCAGACAGGGAGCATCCCTGGTCACTTCAACAACTGTA 122

Qy 1671 -GCGCAAGAGGGCGGCTCAGASCTTGGCACTTGCCACATGGTC--TCCCACAT 1726
Db 121 GCCCCCTGAGACATGGCAGAGGAGGAGTGTCAATGCCACATGATGTCATCCCAGACGT 62

Qy 1727 GGGAGGATCAGCCCGCTGTCACAAATAAGTTATATGAAAAAAA 1786
Db 61 GGGAGGATCAGCACTGCTGTCACATTAACATTATAGTGGAAAAAAAAT 2

Qy 1787 A 1787
Db 1 A 1

RESULT 12
US-09-814-353-2009
Sequence 2009, Application US/09814353
Publication No. US20030165831A1

GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B

CURRENT APPLICATION NUMBER: US/09/814, 353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191, 031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207, 124
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: US 60/211, 940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216, 820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220, 661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257, 672
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2009
LENGTH: 462

Query Match 6.9%; Score 123.2; DB 12; Length 462;
Best Local Similarity 97.7%; Pred. No. 4.6e-28;
Matches 125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1123 CGTAGTCTAATGATTGAGGACATGACTGCCGAATTACATGGCTGATGTCAAGTC 1182
 Db 335 CGTCGTAATGATTGAGGACATGACTGCCGAATTACATGGCTGATGTCAAGTC 394

Qy 1183 TCTTTCCAATGCTCGGATGATGACCTGCTGGTAGCCCCGAAAGCTCTGCAG 1242
 Db 395 TCTTTCCAATGCTCGGATGATGACCTGCTGGTAGCCCCGAAAGCTCTGCAG 454

Qy 1243 AAGAACCC 1250
 Db 455 AAGAACCC 462

RESULT 13
 US-09-814-353-8355
 Sequence 8355, Application US/09814355
 Publication No. US20030165831A1

GENERAL INFORMATION:
 APPLICANT: Thompson, Pamela
 APPLICANT: Lee, John
 APPLICANT: Lillie, James
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF OVARIAN CANCER
 FILE REFERENCE: MRI-006B
 CURRENT APPLICATION NUMBER: US/09/814,353
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: US 60/191,031
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: US 60/207,124
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: US 60/211,940
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: US 60/216,820
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: US 60/220,661
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: US 60/257,672
 PRIOR FILING DATE: 2000-12-21
 NUMBER OF SEQ ID NOS: 22037
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8355
 LENGTH: 462
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 LOCATION: 8
 OTHER INFORMATION: n = A,T,C or G

US-09-814-353-8355

GENERAL INFORMATION:
 APPLICANT: Dillon, Patrick J.
 APPLICANT: Haseltine, William A.
 APPLICANT: Li, Haodong
 APPLICANT: Rosen, Craig A.
 APPLICANT: Rubin, Steven M.
 TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
 FILE REFERENCE: PO-16-2CL
 CURRENT APPLICATION NUMBER: US/09/83,590
 CURRENT FILING DATE: 2000-02-15
 PRIOR APPLICATION NUMBER: 08/420,856
 PRIOR FILING DATE: 1995-04-12
 PRIOR APPLICATION NUMBER: 08/346,731
 PRIOR FILING DATE: 1994-11-21
 NUMBER OF SEQ ID NOS: 12455
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 2528
 LENGTH: 197

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (27)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (33)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (39)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (46)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (63)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (72)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (112)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (118)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (133)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (155)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (177)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (188)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc_feature
 LOCATION: (194)
 OTHER INFORMATION: n equals a,t,g, or c

US-09-783-590-2528

Query Match 5.0%; Score 89; DB 10; Length 197;
 Best Local Similarity 83.2%; Pred. No. 1 8e-17;
 Matches 153; Conservative 0; Mismatches 26; Indels 5; Gaps 5;

Qy 52 AGCCGAGTCGCCGAGATAAGCTCTCCCTTCATCTCTGGGTTCATCACTCACAG 110
 Db 6 ACCCRAAGTCCGCCGAGATAANCTGGNTTAANCCTCTCCCTGGAAATCACTCCANAG 65

RESULT 14
 US-09-783-590-2528
 Sequence 2528, Application US/09783590
 Patent No. US2002010850A1

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RESULT 15
US-09-918-995-8469
; Sequence 8469, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Myseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SBQ ID NO 8469
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-918-995-8469

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Query Match 4.0%; Score 86.6; DB 11; Length 370;
Best Local Similarity 91.1%; Prcd. No. 1.4e-16;
Matches 92; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy 676 CGCACACTGGCCCCGAAATGGACCCCTGACCAAACACTCTGGCATATGACTTCAACAGCTT 735
Db 101 CCCACACTCTTAGGAATGGACCCCTGACCAAACACTCTGGCATATGACTTCAACAGCTT 160
Qy 736 AACTTCTGAGGAGCTCAAGAGAAATCACTCTGGAGACT 776
Db 161 AACTTCTGAGGAGCTCAAGAGAAATCACTCTGGAGAGGT 201

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Search completed: September 22, 2003, 19:19:58
Job time : 330 secs

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GenCore version 5.1.6
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On nucleic - nucleic search, using sw model
Run on: September 22, 2003, 16:58:10 ; Search time 2617 Seconds
(without alignments)

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Maximum Match 0%
Listing first 45 summaries

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Title: US-09-840-704a-1
Perfect score: 1789
Sequence: 1 gaatttcatctgtcgactgct.....aaaaaaaaaaaaaaaaaa 1789

Score: 11 915.8 51.2 994 9 AL55417
12 915 51.1 1201 9 AL528726
13 912.5 51.0 1201 13 BX343152
14 911.6 51.0 1201 13 BX340064
15 909.8 50.9 1201 13 BX340065
16 907 50.7 1201 9 AL569057
17 904.2 50.5 1074 13 BX420812
18 899 50.3 1201 9 AL54330
19 886.4 49.5 1201 13 BX340044
20 884.4 49.4 985 9 AL577921
21 865.4 48.4 1031 12 BM556237
22 864.8 48.3 1201 9 AL520346
23 849.8 47.5 1018 12 BM469734
24 844 47.2 915 13 BQ931548
25 832.4 47.0 974 12 BX340044
26 830.6 46.4 872 13 BU500956
27 829.6 46.4 1201 13 BX332971
28 828.8 46.3 943 13 BX332971
29 824.4 46.1 929 10 BG677948
30 821 45.9 866 12 BM057204
31 815.4 45.6 871 13 BX340044
32 812.6 45.4 840 10 BG685627
33 811.8 45.4 1201 13 BX332971
34 811.4 45.4 901 13 BU190093
35 811.4 45.4 920 13 BQ936739
36 809 45.2 873 13 BQ432354
37 808 45.2 1201 13 BX19993
38 801 44.8 1031 12 BM47530
39 798.2 44.6 829 12 BI820357
40 798.2 44.6 864 14 CD51311
41 791.2 44.2 827 12 BI825570
42 790.6 44.2 934 13 BQ708840
43 790.4 44.2 882 12 CD518757
44 790.2 44.2 1201 13 BX444326
45 787.8 44.0 903 13 BQ672915

Database : EST:
1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estmu:
5: em_estov:
6: em_estapl:
7: em_estro:
8: em_htc:
9: gb_est1:
10: gb_est2:
11: gb_htc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pbn:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_lod:
26: em_gss_phg:
27: em_gss_vrl:
28: gb_gss1:
29: gb_gss2:
SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AK011766
LOCUS
DEFINITION Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610044H13 product:integrin linked kinase, full insert sequence.
ACCESSION AK011766
VERSION AK011766_1
KEYWORDS HTC; GAP trapper;
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
REFERENCE Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning of mouse genes. *Math. Enzymol.* 303, 19-44 (1999)
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL *Genome Res.* 10 (10), 1617-1630 (2000)
MEDLINE 9927923
PUBMED 11042159

REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL *Genome Res.* 10 (10), 1617-1630 (2000)
MEDLINE 9927923
PUBMED 11042159

REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL *Genome Res.* 10 (10), 1617-1630 (2000)
MEDLINE 9927923
PUBMED 11042159

QY 702 GAAACAAACACTCTGGCATGCTCAACACGTTAACCTCCGTGAGCTCAAGAGA 761
 Db 659 GAAACAACACTCCGGATTGCTCAACACTCACTTCGGTCAAGCTCAAGAGA 718
 Qy 762 TCACTCTGGAGAGCTATGGAGGGCGCTSCAGGSCAATGACATATGCGAAGGT 821
 Db 719 TCATTCTGGAGAGCTTGGAGAAGGGCGCTGCAGGGAATATGTTGGAAGCT 778
 Qy 822 GAAGGPTCGAGACTSGAGTAAAGAGAGCAGGACTCATGAGAGCTGCCCGGT 881
 Db 779 GAAGGPTCGAGACTGGAGTAAAGGAAGAGACTTCAATGAGAGCTGCCCGGT 838
 Qy 882 CAGGATTCTCGATCCAAATGTCGCCCCGTCTAGGTCAGTGAAGCTGGAAGGT 941
 Db 839 CAGGATTCTCACACCCCTAACGTGTCCTCGTAGGCTTGCAAGCTGCCAGC 898
 Qy 942 TCTCTCATCTACTCTCATCACACACTGAGTCGCCGTAGGATCTCATGAGGA 1001
 Db 899 CCCACCCACCTCATCACACACTGGATCCATGGATCTCTACATGTCATA 958
 Qy 1002 TGAAGSCACCATTCTGCGGACAGASCAGGCTGAGTTGCTTGACATGCC 1061
 Db 959 TGAAGGCCACCATTCGGTGGAGCAGAGCCTCACAGCTGAGCTCTGACATGGC 1018
 Qy 1062 AGGGCATGCCCTCACACACACTAGAGCCCTCATCCACAGCATGGCTCATAG 1121
 Db 1019 AGAGGCATGCTTCTCCTCACAGCTGAGCTCTCACAGCTGAGCTCACATAG 1078
 Qy 1122 CGTGTAGTGTAAATGATGAGTGTAGGACATGACTGCCAATATGACATGCT 1181
 Db 1079 CGCAGCTGTAATGATGATGAGTGTAGCTGCCCATACTGACATGGTAAATT 1138
 Qy 1182 CTCTTCCAAAGTCGCGTCCATGATGCGCTGCTGGTAGGCCCGAGCTCTGCA 1241
 Db 1139 TCTTTCAGHGCCCTGGCCCATGATGCGCTGCGCTGCGCTGAGCCCTGCA 1198
 Qy 1242 GAAAGAGCTCAAGACACACAGAGCTCGCAGACATGGAGTTGGAGTGTCT 1301
 Db 1199 GAAAGAGCTGAGACACACAGAGCTCGCAGACATGGAGTGTCTGGTCT 1258
 Qy 1302 GTGGGAACTGTGACAGGGGTACCTTGTGACCTCTCCAATATGGAGATGGAT 1361
 Db 1259 GTGGGAACTGTGACAGGGGTACCTTGTGACCTCTXATATGGAGATGGAT 1318
 Qy 1362 GAAGGPGCATGGAGGCCCTCGSCTACCATCCACCGAGTATTCCCTCATGTC 1421
 Db 1319 GAAGGTGGACTGGAGGCCCTCGSCTACCATCCACCGAGTATTCCCTCATGTC 1378
 Qy 1422 TAAGCTCATGAGACTGATGAAGACGCTGAAAGGCCAAATTGACATGAT 1481
 Db 1379 TAAGCTCATGAGATTGATGAGACGCTGAAAGGCCAAATTGACATGAT 1438
 Qy 1482 TGTGCCTATCCCTGAGAGAGCAGACAGTAGGACTGGAGGAGGTCTGCTGACTCC 1541
 Db 1439 TGTGCCTATCTGGAGAGATGAGACAGTAGGACTGGAGGAGGTCTGCAAACTCC 1498
 Qy 1542 AGAGGPTCGAGCTGAGGAGATGCGCTCCACAGCAGGCTCTGGTSC 1601
 Db 1559 CTCCCTGTCCTAATCATGCTGGGGAGTACCTCTCCAAAGTAAAGACCTCTGGTGC 1558
 Qy 1602 CTCCCCGGCTCCAGTGTACCCCGG-CCTGGGTGTCATCCCTTCCCATCC 1660
 Db 1599 AGAAGTGTCAAACATGCTGGGGAGTACCTCTCCAAAGTAAAGACCTCTGGTGC 1618
 Qy 1661 CTACCACTGT---GCCAAGAGGGGGCTGAGGTTGCACTGCCATGGTC 1717
 Db 1619 CTACCACTGTGCCCCAAAGGGCTGGCTGAGCTTGTCACTGCCATGGTC 1678
 Qy 1718 TCCCAACATGGAGGATCAGCCCGCTGCAATAAGTTTAT 1766
 Db 1679 TCCCAACATGGAGGATCAGCCCGCTGCAATAAGTTTAT 1727

REFERENCE	RESULT 2
AUTHORS	AK002344
DEFINITION	AK002344 1705 bp mRNA linear HTC 05-DEC-2002
LOCUS	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:061008K16 product:integrin linked kinase, full insert sequence.
ACCESSION	AK002344
VERSION	AK002344.1 GI:12832253
KEYWORDS	HTC; CAP trapper
SOURCE	Mus musculus (house mouse)
ORGANISM	Fukuyama; Metacea; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butcheria; Rodentia; Sciurognath; Muridae; Murinae; Mus
REFERENCE	Carninci, P. and Hayashizaki, Y.
AUTHORS	High-efficiency full-length cDNA cloning
TITLE	Meth. Enzymol. 303, 19-44 (1999)
JOURNAL	99279253
MEDLINE	10349636
PUBMED	2
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okezaki, Y., Muramatsu, M. and Hayashizaki, Y.
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
TITLE	Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL	20499374
MEDLINE	11042159
PUBMED	3
REFERENCE	Shibata, K., Itoh, M., Aizawa, Y., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishimi, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneida, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuo, S., Kawai, J., Orazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
AUTHORS	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
TITLE	Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL	20530913
MEDLINE	11076861
PUBMED	4
REFERENCE	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, F., Hara, A., Fukunishi, K., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okaaki, T., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, T., Matsuda, H., Ashburner, M., Batyalov, S., Cabavant, T., Fleischmann, R., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Built, C., Fletcher, C., Fujita, M., Garibaldi, M., Guetinichich, S., Hill, D., Hoffmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombart, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Storch, K.F., Suzuki, H., Toyoda, K., Wang, K.H., Weitz, C., Whittaker, C., Wimbing, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
AUTHORS	Functional annotation of a full-length mouse cDNA collection
TITLE	Nature 409 (6821), 685-690 (2001)
JOURNAL	2108560
MEDLINE	11217851
PUBMED	5
REFERENCE	The RIKEN Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
TITLE	Nature 420, 563-573 (2002)
JOURNAL	6 (bases 1 to 1705)
REFERENCE	Arakawa, T., Bono, H., Carninci, P., Akimura, T., Arai, A., Aono, H.,
AUTHORS	Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraiwa, T., Hori, F., Imoto, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibusawa, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, T., Takanashi, F., Tanaka, T., Teijima, Y., Tera, T., Yamada, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.	Qy 282 CGAGAGGGCCGCTCTGCTGAGATCTGGATCATGGGGCACGGATCAATGT 341 Db 219 CGAGAGGGCGCTCTGGTGAATCTGTGATCATGGAGACGGATATGT 278
TITLE Direct Submission	Qy 342 AATGAAACCGTGGGATGACACCCCTGCATCTGGCAGGACCGTGATAT 401 Db 279 GATGAATGTTGGATGATACCCCTGACACTGCGACGTAGTCATGGACAT 338
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-re@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	Qy 402 TGTACAGAAGCTATTGAGTACAAGGAGACATCATGAGTGAATGAAACGGGAATGT 461 Db 339 TGTACAGAAGCTGTGCAATACAAAGGCTGACATGAGTGAATGAGTGAATGT 398
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.	Db 462 GCCCCCTGCACTATGCCCTGTTGGGCCAACAGATAAGTCAGGAGGACCTGGTGCAAA 518 Qy 399 GCCAATCTCATATGGATGTTCTGGGCCAACAGACAGGACCTGGTGCATA 458 Db 519 ACCCTTCTAGAGCTTCTCCGAAACGGGAGAGAAATGGCCGAAATCTCACCGTAT 578
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Location/Qualifiers 1..1705	Qy 582 ACCCTCTGAGAGCTTCTCCAGAGGGAGAGAGATGGCCGAATCTCACCGTAT 641 Db 519 ACCCTTCTAGAGCTTCTCCGAAACGGGAGAGAAATGGCCGAAATCTCACCGTAT 578
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misc_feature	Qy 1122 CCGTGTGTGATGTTGATGTTGATGAGTGGCTGATGTCAGTTGAACTT 1181 Best Local Similarity 89.6%; Pred. No. 4.2e-194; Mismatches 0; Indels 167; Gaps 4;
Matches 1496; Conservative	Db 1058 CGCGACTGTATGATGATGAGATGATGTCATGTTGAACTGTTGAACTT 1117
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polyA_signal	Qy 162 CGACATTTCACTGCGGGAGGCGCAAGCGCACTGGCTGTGCTGTGATGGA 221 Db 99 CGACATTTCACTGCGGGAGGCGCAAGCGCACTGGCTGTGCTGTGATGGA 158
polyA_site	Qy 222 CACGGAAACGACCTAACCAAGGGGACGATCATGGCTCTCCCTTGGACTGGCCCTG 281 Db 159 CACAGAAACGACCTAACCAAGGGGATGATGGCTCTCCCTTGGACTGGCCCTG 218
BASE COUNT ORIGIN	Qy 1302 GTGGGAACCTGTTGAGTACGGGAGGTTACCTCTGCTACATGGAGATGGATGGAT 1361 Db 1238 GTGGGAACCTGTTGAGTACGGGAGGTTACCTCTGCTACATGGAGATGGATGGAT 1297

Query Match 54 7%; Score 979 4; DB 9; Length 1201;
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ORIGIN

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 Qy 1661 CTACCACTGTT---GCCAAGGGGGGGCTCAGCTTGTCACTTGCCACATGGTGC 1717
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 Db 849 GAGTKTCGCCGGCTCAGGATTCTCGCATCCAAATGTCCTCCAGTGTAGGTGCTGC 927
 Db 909 KICKTGAGGTTGCTGAGGTGAGACTGGGATCAAGGGAGAGGAGGGACTCTCG 850
 Qy 868 GAGTGTCCCGCTCAGGATTCTCGCATCCAAATGTCCTCCAGTGTAGGTGCTGC 927
 Db 928 CAGTCCTCACCTGCTCCATCTACTCTCATCACACACTGGATGCCATGGATCCCTC 987
 Db 789 CAGTCCTCACCTGCTCTCATCTACTCTCATCACACTGGATCCATGGATCCCTC 730
 REFERENCE
 Qy 988 TACAATGCTACTACATGAGGCCAACATTGCTCGGGACCAGGCCAGGGCTGTGAGTT 1047
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 16, 2001 this sequence version replaced gi:12945092.
 Contact: Genoscope
 Genoscope - Centre National de Sequencing
 BP 191 91006 EVRY cedex - France
 Email: secrete@genoscope.cns.fr Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f For more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/clusser.cgi?seq=CS00J003BF09NP1&cluster=6100.f>. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS00J003BF09NP1.

FEATURES

source 1. -1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /note="1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Eco V sites of the PCMVSPORT 6 vector. Library was normalized."

BASE COUNT

257 a 281 C 318 g 301 t 44 others

Qy	1586	GCAGGGCTCTGGTGGCTCCCCGCTCAGTCATGGACTA--CCCAAGCTGGGTCC	1643		Qy	841	ACAAGGAAGGACGGGACTCAATGAAAGTGTCCCCGGTCAGGATTTCTGGATCCA	900
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Db	70	ATCCCCCTCCCATCCACTTCACTCTGCCCCAACAGGGGGCTCAGAGCTTGTC	11		Db	305	AATGTCGCTCCAGCTAGGTGCCAGTCTCCACCTGCTCCATCTCAGCTCATC	364
Qy	1702	CTTGCCACAT 1711			Qy	961	ACACACTGGATGGCGGTAGATCCCTACAAATGFACTACATGAGGCCAAATTCTGTC	1020
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Qy		RESULT 4			Qy	1021	GTGGACAGAGGCCAGCTGTGAAAGTTGGCATGGCAAGGGCATGGCTTCCTA	1080
AL528727	AL528727	1201 bp mRNA linear EST 23-MAY-2003			Db	425	GTGGACAGAGGCCAGCTGTGAAAGTTGGCATGGCAAGGGCATGGCTTCCTA	484
LOCUS	AL528727	Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens			Qy	1081	CACACACTAGAGCCCCATCCCAGACATGCACTAATAGCCGTAGTGTAAATGATTGAT	1140
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ACCESSION	AL528727	EST.			Qy	1141	GAGGACATGACTGCGCAATTAGCCTGGCTGATGTCAGTCTTCCAAATGTCCTGGT	1200
VERSION	AL528727.2	GI: 310665777			Db	545	GAGGACATGACTGCGCAATTAGCCTGGCTGATGTCAGTCTTCCAAATGTCCTGGT	604
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REFERENCE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Qy	1261	AACAGACGCTCAGCACACATGGAGTTTGCACTGCTCTGTGGAAACTGTGACACGG	1320
AUTHORS		Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			Db	665	AACAGACGCTCAGCACACATGGAGTTTGCACTGCTCTGTGGAACTGTGACACGG	724
TITLE		Full-length cDNA libraries and normalization			Qy	1321	GAGGATACCCCTTGCAGACCCCTCCATAATGGAGATGGATGAGTGTGGGATTGGAGGC	1380
JOURNAL		Unpublished			Db	725	GAGGATACCCCTTGCAGACCCCTCCATAATGGAGATGGATGAGTGTGGGATTGGAGGC	784
COMMENT		On Feb 13, 2001 this sequence version replaced gi:12792220.			Qy	1381	CTTCGGCCTACATCCACAGGTTCCTCCCTCATGTAACCTCATGAGATCTGC	1440
		Contact : Genoscope - Centre National de Sequenage			Db	785	CTTCGGCCTACCCATCCACAGGTATTCCCTCTGGTAGACTCATGAGATCTGC	844
		BP 191 91006 EVRY cedex - France			Qy	1441	ATGAATGAAGGCCCTSCAACGACCCAAATTGACATGATTGTGCTCATCTTGGAAAG	1500
		Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr			Db	845	ATGAATGAAGGCCCTSCAACGACCCAAATTGACATGATTGTGCTCATCTTGGAAAG	904
		Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f. For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODD001BF09QP1&cluster=6100.f. Contact : Feng Liang Email: fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODD001BF09QP1.			Qy	1501	ATGCAGGACAGTAGGACTGCGCTTCACCTCGAGCTGGGAATGATGGT	1560
FEATURES		Location/Qualifiers			Db	905	ATGCAGGACAGTAGGACTGCGCTTCACCTCGAGCTGGGAATGATGGT	964
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		/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Eco R sites of the pCMVSPORT 6 vector. Library was normalized."			Qy	1740	CCGGCTGTCACTGACCTGGCTCATCCCTTCACATGTC	1787
BASE COUNT	317	a 305 c 297 t 257 g			Db	1132	ASCCCGCTKTTAAATTWWTGAAAAAANNNWDW 1179	
ORIGIN		Query Match 54.5%; Score 974.4; DB 9; Length 1201; Best Local Similarity 92.9%; Pred. No. 1.5e-137; Matches 1048; Conservative 17; Mismatches 49; Indels 14; Gaps 4;			RESULT 5			
		Qy	661	TGGAAAGGGGACCAACCCCCACTGGCCCCGAAATGGACAAACACTCTGGCAT	720	AL579748 LOCUS AL579748 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED	1201 bp mRNA linear EST 01-JUN-2003	
		Db	65	TGGAAAGGGGACCAACCCCCACTGGCCCCGAAATGGACAAACACTCTGGCAT	124	DEFINITION Homo sapiens clone CSODD001YK18 5'-PRIME, mRNA sequence.		
		Qy	721	GACTTCAAACACCTTAACCTCTGACTCAACGGAATCACTCTGGAGGTATGG	780	ACCESSION AL579748		
		Db	125	GACTTCAAACACCTTAACCTCTGACTCAACGGAATCACTCTGGAGGTATGG	184	VERSION AL579748		
		Qy	781	AAGGGCCGCTGGCAAGGCAATGACATGGTCTGAAAGGTGCTGAAAGCTGGAGT	840			
		Db	185	AAGGGCCGCTGGCAAGGCAATGACATGGTCTGAAAGGTGCTGAAAGCTGGAGT	244			

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	
REFERENCE	
AUTHORS	Li, W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	On Feb 16, 2001 this sequence version replaced gi:12945094.
FEATURES	Contact: Genoscope
source	Genoscope - Centre National de Sequencage
BASE COUNT	BP 191 9106 EVRY cedex - France
Match	Email: segr@genoscope.cns.fr, Web : www.genoscope.cns.fr
Matches 1005	library was constructed by life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f For more information about this cluster, see
	http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS00J003BF09QPI&cluster=6100.f .
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	/note="1st strand cDNA was primed with a NotI-oligo(dN) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library was normalized."
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ORIGIN	
Query Match	54.1%; Score 968.6; DB 9; Length 1201;
Best Local Similarity	98.4%; Pred. No. 1.1e-136;
Matches 1005	4; Mismatches 8; Indels 4; Gaps 3;
QY	
Db	36 CGGAGAGGATCTGCAGCCGAGTCGCCGAGATAAAGCTGGGTICATCCTCCCTCCC 95
QY	22 CGGAGAGGATCTGCAGCCGAGTCGCCGAGATAAAGCTGGGTICATCCTCCCTCCC 81
QY	96 TGGATCACTCCACAG-TCTCGAGGCTTCCCCTAACCCAGGACTCGGCAGGGAGCTG 154
Db	82 TGGATCACTCCACAG-TCTCGAGGCTTCCCCTAACCCAGGACTCGGCAGGGAGCTG 141
QY	155 CTATGGACGAACTTCACTCGAGTGGGGGCAACGCGCTCGCGCTGGCTTG 214
Db	142 CTATGGACGAACTTCACTCGAGTGGGGGCAACGCGCTCGCGCTTG 201
QY	215 TGGACACACCGAGAACGACCTCAACCGGGGACCATCATGGCTCTCCCTGCACT 274
Db	202 TGGACACACCGAGAACGACCTCAACCGGGGACCATCATGGCTCTCCCTGCACT 261
QY	275 GGGCTTCCGAGGGCGCTCTGCTGTTGAGATGTTCACTCGGGGGGACGGA 334
Db	262 GGGCTTCCGAGGGCGCTCTGCTGTTGAGATGTTCACTCGGGGGGACGGA 321
QY	335 TCAATGTAATGACCGTGGGATGACCCCTGATCGTGGAGGAGCTGATGACCC 394
Db	322 TCAATGTAATGACCGTGGGATGACCCCTGATCGTGGAGGAGCTGATGACCC 381
QY	395 GTGATATGAGAAGCTATGAGTACAAGGAGCATGATGAGTGAACG 454
Db	382 GTGATATGAGAAGCTATGAGTACAAGGAGCATGATGAGTGAACG 441
QY	455 GGAATGTCGCCCTGCACTATCCTGTTGGGCCAGATGAGTCAAGGGAGCTG 514
FEATURES	Location/Qualifiers
RESULT	6
LOCUS	AL528726
DEFINITION	1201 bp mRNA linear EST 23-MAY-2003
ACCESSION	AL528726 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS00D01YK18 3'-PRIME, mRNA sequence.
VERSION	AL528726.2 GI:31066576
KEYWORDS	EST.
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	
AUTHORS	Makrilia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	On Feb 13, 2001 this sequence version replaced gi:12792219.
FEATURES	Contact: Genoscope
source	Genoscope - Centre National de Sequencage
BASE COUNT	BP 191 9106 EVRY cedex - France
Match	Email: segr@genoscope.cns.fr, Web : www.genoscope.cns.fr
Matches 1005	library was constructed by life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f For more information about this cluster, see
QY	http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS00D01BF09NP1&cluster=6100.f .
Db	Feng Liang Email : fliang@litech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CS00D01BF09NP1.
LOCUS	Location/Qualifiers

source	1. . 1201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DD001YK18" /issue_type="NEUROBLASTOMA COT 50-NORMALIZED" /clone_id="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." BASE COUNT 258 a 299 c 314 g 36 others	Qy 1502 TGCAGGACAAAGTAGGACTGGAAAGGCCCTGCCTGAACCTCCAGGGACATGGTT 1561 Db 262 TGCAGAACAGTAGGACTGGAAAGGCCCTGCCTGAACCTCCAGGGACATGGTT 203	
		Qy 1562 GGGGAATGACCTCCTGCTGCTCCCTCCAGGGACTCCAGTCATG 1621 Db 202 GGGGAATGACCTCCTGCTGCTCCCTCCAGGGACTCCAGTCATG 143	
		Qy 1622 GTACTTACCCAGCC-TGGGTCCATCCCCATCCCTACCACTGTG--CCAAAGA 1678 Db 142 GTACTTACCCAGCC-TGGGTCCATCCCCATCCCTACCACTGTG 83	
		Qy 1679 GGGGGGGCTGACAGCTTGCACTGGCATGGGGATCAG 1738 Db 82 GGGGGGGCTGACAGCTTGCACTGGCATGGGGATCAG 24	
Query Match Best Local Similarity 95.5%; Pred. No. 5.8e-136; Matches 1053; Conservative 11; Mismatches 30; Indels 9; Gaps 7;		Qy 1739 CCCCGCTGTACATAAAAGTT 1761 Db 23 CCCCGCTGTACATAAAAGTT 1	
		RESULT 7 AL526689 LOCUS AL528689 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens DEFINITION CDNA clone CS0DD001YK05 5'-PRIME, mRNA sequence. AL528689 Db 1039 CTYCACACCGTTRACCTCCCTGAGAGCTGAGATTA 1040 Qy 723 CTTCACAAACGCTTAACCTCTGAGAGTAATCTGGAGGTATGGA 781 Db 1098 GAAAGGAAACCCACCCGAAATGGAAACAAACACTCTGGATTGA 722 Qy 663 GAGGGGACACCACCCGACTCGGCCCGAACATGGAAACAA 941 Db 1098 GAAAGGAAACCCACCCGAAATGGAAACAAACACTCTGGATTGA 1040 Qy 782 AGGGCCGCTGGCAGGGCAATGACATGTCGTGAAGGGTTCGAGACTGGAGTA 980 Db 979 A-GGCCCTGGAGGGAAATGGTGTGAGGTGAACTGGAGTA 921 Qy 842 CAAGGAAGGAGGGACTCAATGAAGAGCTCTCGCATCCAA 901 Db 920 CAAGGGAGGGAGGGACTCAATGAGAGCTCTCGCATCCAA 861 Qy 902 ATGTGCTCCAGTGTAGTGTAGTGTCTGCACGTCATCCTACTCTCA 961 Db 860 ATGTGCTCCAGTGTAGTGTAGTGTCTGCACGTCATCCTACTCTCA 801 Qy 962 CACACTGATGCCGTATGATGCCCTCTAACATGTACTACATGAAGGCCAAATTCGTGCG 1021 Db 800 CACACTGATGCCGTATGATGCCCTCTAACATGTACTACATGAAGGCCAAATTCGTGCG 741 Qy 1022 TGGACCAAGGAGCCGGCTGTGAAGGTGCTTGGACATGGCAAGGGCATGCTCTCTAC 1081 Db 740 TGGACCAAGGAGCCGGCTGTGAAGGTGCTTGGACATGGCAAGGGCATGCTCTCTAC 681 Qy 1082 ACACACTGAGCCCTATCCAGGAGCTGAGCTGCTTGGACATGGCAAGGTGATGATGATG 1141 Db 680 ACACACTGAGCCCTATCCAGGAGCTGAGCTGCTTGGACATGGCAAGGTGATGATGATG 621 Qy 1142 AGGACATGACTGCCGAATTAGCATGGCTGATGTCAGTTGGACATGGCAAGGTGATGATG 1201 Db 620 AGGACATGACTGCCGAATTAGCATGGCTGATGTCAGTTGGACATGGCAAGGTGATGATG 561 Qy 1202 GCATGTGATGCCGAATTAGCATGGCTGATGTCAGTTGGACATGGCAAGGTGATGATG 1261 Db 560 GCATGTGATGCCGAATTAGCATGGCTGATGTCAGTTGGACATGGCAAGGTGATGATG 501 Qy 1262 ACAGACCTCAGCAGACATGGGAGTTGGAAACTGGTCTGTGGAACTGGTCTGTGGGG 1321 Db 500 ACAGACCTCAGCAGACATGGGAGTTGGAACTGGTCTGTGGGGACTGGTCTGTGGGG 441 Qy 1322 AGTACCTCTTGTGACCTCTCAAAATTGGAGATGGAGATGGAGATGGAGGCC 1381 Db 440 AGTACCTCTTGTGACCTCTCAAAATTGGAGATGGAGATGGAGGCC 383 Qy 1382 TTGGGCTTACCATCCACAGGTTGGGAACTGGTCTGTGGGGACTGGTCTGTGGGG 1441 Db 382 TTGGGCTTACCATCCACAGGTTGGGAACTGGTCTGTGGGGACTGGTCTGTGGGG 323 Qy 1442 TGAATGAAAGACCCCTGCAAAGGGACCCAAATTGGACATGATGGCTATCCTTGAGAAGA 1501 Db 322 TGAATGAAAGACCCCTGCAAAGGGACCCAAATTGGACATGATGGCTATCCTTGAGAAGA 263	Query Match 53.3%; Score 952.8; DB 9; Length 1201; Best Local Similarity 97.1%; Pred. No. 2.6e-134; Matches 981; Conservative 9; Mi.matches 16; Indels 4; Gaps 2; Qy 108 CAGTCTCAGGCTTCCCCAACTCCAGGGACTCGGGCCGGACGCTGCTATGGAGACAT 167 Db 116 CGGTCTCAGGCTTCCCCAACTCCAGGGACTCGGGCCGGACGCTGCTATGGAGACAT 175

	KEYWORDS	EST.
	SOURCE	Homo sapiens (human)
	ORGANISM	
Qy	TTTCACTCAGTGCCGGAGGCCAACCGTCAGTGCCTGCTGCTGGCTGAAACACGGA	227
Db	TTTCACTCAGTGCCGGAGGCCAACCGTCAGTGCCTGCTGCTGGCTGAAACACGGA	235
Qy	228 GAAAGACTCACCAGGGGAGATCATGGTTCCCTCTGACTGGGCTGGAGA	287
Db	GTACGACCTCACACAGGGGAGATCATGGCTCTGACTGGGCTGGAGA	295
Qy	288 GGGCCCTCTGCTGTTGAGATGTGATGATGATGATGAA	347
Db	GGGCCCTCTGCTGTTGAGATGTGATGATGATGATGAA	355
Qy	296 GAAAGCTTGTGTTGAGATGTGATGATGATGAA	355
Db	CGTGGGATCACACCCCCCTGCATCTGGGCCAGTCAGTGCACCGTGTATGTACA	407
Qy	348 CGTGGGATCACACCCCCCTGCATCTGGGCCAGTCAGTGCACCGTGTATGTACA	407
Db	CGTGGGATCACACCCCCCTGCATCTGGGCCAGTCAGTGCACCGTGTATGTACA	415
Qy	356 CCGTGGGATCACACCCCCCTGCATCTGGGCCAGTCAGTGCACCGTGTATGTACA	415
Qy	408 GAAAGCTTGTGTTGAGATGTGATGATGATGAA	467
Db	416 GAAGCTTGTGTTGAGATGTGATGATGAA	475
Qy	468 GCACTATGCCCTGGGCCAACATCAAGGAGACATCAATGCACTGAGAATGAGGAAATGGGC	527
Db	GCACTATGCCCTGGGCCAACATCAAGGAGACATCAATGCACTGAGAATGAGGAAATGGGC	535
Qy	476 GCACTATGCCCTGGGCCAACATCAAGGAGACATCAATGCACTGAGAATGAGGAAATGGGC	535
Db	CCTGTCAGCTCTGAAACAGTATGCTGAGAGATGCTGTCACAAAGCCAGGGACCCCT	587
Qy	536 CCTGTGAGCTCTGTCAGATGATGAGATGCTGTCACAAAGCCAGGGACCCCT	595
Qy	588 GAGAGAGCTTCTCGAGAGGGGAGAGAGATGGCCAGATCAGCTAACCTTCCATA	647
Db	GAGAGAGCTTCTCGAGAGGGGAGAGAGATGGCCAGATCAGCTAACCTTCCATA	655
Qy	648 CAAGGACACATCTGAAAGGGGACACCCGGACTCGCCCGAAATGAAACCTGAAACA	707
Db	CAAGGACACATCTGAAAGGGGACACCCGGACTCGCCCGAAATGAAACCTGAAACA	715
Qy	656 CAAGGACACATCTGAAAGGGGACACCCGGACTCGCCCGAAATGAAACCTGAAACA	715
Db	708 ACACCTGGCTTGACTTCACACASCTTAACCTCTGACGAGCTAACGGAATCACTC	767
Qy	716 ACACCTGGCTTGACTTCACACASCTTAACCTCTGACGAGCTAACGGAATCACTC	775
Db	768 TEGAGAGCTTGTGAAAGGGCCCTGGAGGGAAATGAGCTTCTGAAAGGTCTGAAAGT	827
Qy	776 TEGAGAGCTTGTGAAAGGGCCCTGGAGGGAAATGAGCTTCTGAAAGGTCTGAAAGT	835
Db	828 TGGAGACTGAGTACAGGAAGAGGAGCTCAATGAAGAGTGTCCACCTGCTCTCA	887
Qy	836 TGGAGACTGAGTACAGGAAGAGGAGCTCAATGAAGAGTGTCCACCTGCTCTCA	895
Db	888 TTTCCTGCATCTCAATGTGCTCCAGTGCTCTGAGATCTCTGAGCTTCTGAAAGG	947
Qy	896 TTTCCTGCATCTCAATGTGCTCCAGTGCTCTGAGCTTCTGAAAGG	955
Db	948 TCTACTCTCATCACACACTGATGCTCTCATGACTACATGAAAGG	1007
Qy	956 TTCTACTCTCATCACACACTGATGCTCTCATGACTACATGAAAGG	1015
Db	1008 GACCAATTCTGTCGAGCAGGAGCCAGGTGTGAAGTTCCTTGACATGGCAAGGG	1067
Qy	1015 GACCAATTCTGTCGAGCAGGAGCCAGGTGTGAAGTTCCTTGACATGGCAAGGG	1075
Db	1068 CATGGCCTCTCACACACTAGASGCCCTATCCACAGGAGATGACTCA	1117
Qy	1076 -ATGGCCTCTCACACACTAGAGCCC-TCATCCACAGGAGATGACTCA	1121
RESULT 8		
AL581548/c	AL581548 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA clone CS0DG004Y019 3'-PRIME, mRNA sequence.	1201 bp linear EST 01-JUN-2003
DEFINITION		
ACCESSION	AL581548	
VERSION	AL581548.2	GI:31319788
FEATURES		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
CONTACT		
Genoscope - Centre National de Sequençage		
BPN 191 91006 EVRY cedex - France		
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f. For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DG004AH10NP1&cluster=6100.f. Contact : Feng Liang Email: filiang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope Sequence ID : CS0DG004AH10NP1.		
BASE COUNT		
ORIGIN		
Query Match	52.8%	Score 944; DB 9; Length 1201;
Best Local Similarity	94.3%	Pred. No. 5.6e-133;
Matches	1013;	Conservative 14; Mismatches 41; Indels 6; Gaps 5;
Db	674 CCCGACCTCGCCCCGAAATGAAACACCTGACACAAACCTGGCATGACTTCACAGC	733
Qy	1071 CCCCCCCACCYVGCCCCRAATKGACACCTGACACAAACAYTCTGGATT-ACTTCACACG	1013
Db	734 TTAACCTCTGACGAGCTAACGAACTCTGGAGAGCTATGGAAAGGGCCCTGG	793
Qy	1012 TTAACTCTGMC-AAGCTAACAGAATCACTCTGGAGAGCTATGGAAAGGGCCCTGG	954
Db	794 AGGGCAATGACATGGTGTGAAGGTTGTGAAGGTTGTGAAGTACAGGAAGGCA	853
Qy	953 AGGGCAATGACATGGTGTGAAGGTTGTGAAGTACAGGAAGGCA	894
Db	854 GGGCACTCAATGAAAGTGTGCCCCGCTCAGGATTCTGGCATCCAATGTGTCCAG	913
Qy	893 GGACATCTCATGAAAGTGTGCCCCGCTCAGGATTCTGGCATCCAATGTGTCCAG	834
Db	914 TGTCTGGCTGCAGTCACCTGCTCTCATCTCATCACACACTGGATGTC	973
Qy	833 TGCTAGTGTGCTGCCAGTCACCTGCTCTCATCTCATCACACACTGGATGTC	774
Db	974 CGTATGGATCCTACATGACTACATGAGGGCACATTCTGCTGAGGACCAAGCAATTCTGCTGAGGAGGCC	1033
Qy	773 CGTATGGATCCTACATGACTACATGAGGGAGGCC	714
Db	1034 AGGCTGTAAGTGTCTTGACATGCGAAGGGCATGGCCTCTACACACTAGAGC	1093
Qy	713 AGGCTGTAAGTGTCTTGACATGCGAAGGGCATGGCCTCTACACACTAGAGC	654
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		/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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		/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with N1 and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
Db	653	CCCTCATCCAGACATGCACTAA TAGCCGTAGTGTAATGATTGAGGACATGACTG 594
Qy	1154	CCCGAATTAGCATGGCTTCACTTCTGCACTTCATGCTCTGCCTGATGCCATGATGCCAC 1213
Db	593	CCGAATTAGCATGGCTTCACTTCTGCACTTCATGCTCTGCCTGATGCCAC 534
Qy	1214	CNGCTGGTAGCCCCGGAGCTCTGCAAGAACAGCTGAAGACAACAGACGCTAG 1273
Db	533	CTGCCCTGGTAGCCCCGGAGCTCTGCAAGAACAGCTGAAGACAACAGACGCTAG 474
Qy	1274	CAGACATGGAGGTTTCTGAGTGACACGGAGGTACCCTTG 1333
Db	473	CAGACATGGAGGTTTCTGAGTGACACGGAGGTACCCTTG 414
Db	1334	CTGACCTCTCCAATATGGAGATGGATGAGCTGGCTTGGCTTACCA 1393
Qy	413	CTGACCTCTCCAATATGGAGATGGATGAGCTGGCTTACCA 356
Db	1394	TCCACAGGATTCCCTCATGTTGTAAGATCTGCAATGATGAGACC 1453
Qy	355	TCCACCCGGATTCCCTCATGTTGTAAGATCTGCAATGATGAGACC 296
Db	1454	CTGCAAAGGACCCAAATTGACATGATGTTGCTTATCCTGAGAATGGAGGAAGT 1513
Qy	295	CTGCAAAGGACCCAAATTGACATGATGTTGCTTATCCTGAGAATGGAGGAAGT 236
Qy	1514	AGGACTGGAAAGTCCCTGGCAACTCCAGAGGTCTGGGACATGGTTGGGAATGCA 1573
Db	235	AGGACTGGAAAGTCCCTGGCAACTCCAGAGGTCTGGGACATGGTTGGGAATGCA 176
Qy	1574	CTCCCCAAAGCGCCTGGCTTCCCGCCCTCAGTCATGTTACTACCCAG 1633
Db	175	CTCCCCAAAGCGCCTGGCTTCCCGCCCTCAGTCATGTTACTACCCAG 116
Qy	1634	CC-TGGGTCCTCATCCCTTCCCCTCACTCT-GCCAAAGGGGGGCTAG 1691
Db	115	CCATGGGTCCATCCCTTCCCCTCCMCAIMMHACACTGGGCCAAGGGGGCTAG 56
Qy	1692	ACGTTTGCACTTGCCACATGGGAGGATCACAGCCGGCC 1745
Db	55	ACGTTTGCACTTGCCACATGGGAGGATCACAGCCGGCC 2
RESULT	9	BX332970/c
LOCUS	BX332970	1200 bp mRNA linear EST 01-MAY-2003
DEFINITION		Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
ORGANISM		
COMMENT		
REFERENCE	Li, W.B., Gruber, C.J., Jesse, J., and Polayes, D.	
AUTHORS		
JOURNAL		
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
COMMENT	Full-length cDNA libraries and normalization	
CONTACT	Genoscope	
COMMENT	Genoscope - Centre National de Séquençage	
REFERENCE	BP 191 9106 ERY cedex - France	
JOURNAL	Email: segenfogenoscope.cns.fr, Web : www.genoscope.cns.fr	
KEYWORDS	Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f. For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODC017DD10NP1&cluster=6100.f. Contact : Feng Liang Email : fliang@lilletech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genscope sequence ID : CSODC017DD10NP1.	
FEATURES	source	1. 1200

QY 1513 TAGGACTGGAAAGGTCTTGCGTGAACCTCCAGGGCTCTGGGACATGGTGGGGATGCA 1572
 Db 212 TAGGACTGGAGGTCCTTGCGTGAACCTCCAGGGCTCTGGGACATGGTGGGGATGCA 153
 QY 1573 CCTCCCCAACAGCAGCAGGCCCTGGTGCCTCCCGCCCTACAGTCATGTTACCCCA 1632
 Db 152 CCTCCCCAACAGCAGCAGGCCCTGGTGCCTCCCGCCCTACAGTCATGTTACCCCA 93
 QY 1633 CCC-TGGGRCATCCCTTCCCCTCCCTACCACTGTG-CGAAAGGGGGCTC 1689
 Db 92 GCGATGGGTCTATCCCTTCCCCTACACTGTGAGGAGGGGCTC 33
 QY 1690 AGAGCTTGTACTGCCACATGGTCTCC 1721
 Db 32 AGAGCTTGTACTGCCACATGGTCTCC 1
 RESULT 10
 AL559057/c AL569057 Homo sapiens 1201 bp mRNA linear EST 13-MAY-2003
 LOCUS DEFINITION AL569057 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE003YD17 3'-PRIME, mRNA sequence.
 ACCESSION AL569057
 VERSION A1569057.2 GI:30605114
 KEYWORDS EST:
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Li,W.B., Gruber,C., Jessie,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization.
 JOURNAL Unpublished
 COMMENT On Feb 16, 2001 this sequence version replaced gi:12924017.
 Contact: Genoscope
 Genoscope - Centre National de Séquençage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f. For more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODE003CB09NP1&cluster=6100.f>. Contact : Feng Liang Email: fliang@lifetech.com URL : <http://FullLength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODE003CB09NP1.

FEATURES
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 1. -1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone_Tbs="Homo sapiens PLACENTA"
 /note="vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized."
 BASE COUNT
 ORIGIN 245 a 296 C 323 G 295 T 41 others
 Query Match 52.3% Score 935 DB 9 Length 1201; Best Local Similarity 93.2%; Pred. No. 1.3e-131; Matches 1007; Conservative 20; Mismatches 45; Indels 8; Gaps 5;
 QY 649 AAGGACACATTCTGAGGGGACACCCGACTGGCCCAAATGAAACCCGTGACAA 708
 Db 1087 AAAAGACAMATYTGAAAGGCCAACCGCGC-CGCGCGAAGTGAACCAA 1029
 QY 709 ACTCTGGCATGTACTCAACAGCTTAACCTCTGAGAAGCTAACGAGGATCACT 768
 Db 1028 TTCT--GCATGACTTCAMACAGCTTAACCTCTGAGAAGCTACCGAGAACTCT 972

RESULT 11
 AL555417 AL555417 Homo sapiens HELA CELLS 994 bp mRNA linear EST 31-MAY-2003
 LOCUS DEFINITION AL555417 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens cDNA clone CSODK008Y014 5'-PRIME, mRNA sequence.
 ACCESSION AL555417
 VERSION A1555417.2 GI:3127724

QY 769 GGAGAGCTATGGAAGGGCCCTGGAGGCAATGACATGTCGAAGGTGCTGAAGTT 828
 Db 971 GGAGAGCTATGGAAGGGCCCTGGAGGCAATGACATGTCGAAGGTGCTGAAGTT 912
 QY 829 CGAGACTGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 888
 Db 911 CGARACTGGAGWACAGGAAGAGCAGGACTTCATGAGAGTGTCCCGCTCAGATT 852
 QY 889 TTCTGGCATCCAATGTCGCCAGTCTAGTGCTGCGTGCAGTCACCTGCTCAT 948
 Db 851 TTCTGGCATCCAATGTCGCCAGTCTAGTGCTGCGTGCAGTCACCTGCTCAT 792
 Db 791 CCTACTCTCATCACACTGATGCGTATGGATCCCTACATGTAATGAGGC 732
 QY 1009 ACCAATTCTCTGAGGAGAGCCAGCTGCTGAGTTCTTGGACATGGCAAGGGC 1068
 Db 731 ACCAATTCTCGTGTGAGCCAGGCGAGCTGTGAATGGCAATGGCAAGGGC 672
 QY 1069 ATGGCCTCTACAGACACTAGAGGCCCTCATCCACAGACATGACTCAATGGCTGT 1128
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 QY 1129 GTAAATGATGAGGAGCATGACTGCCGATAATGGTAGCTGTGAGTCAAGTCCTTC 1188
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 QY 1369 GCATTTGAAAGGCCCTTGCCCTACCATCCACCGAGCTTGCAGTGTCTGGGAA 1428
 Db 371 GCATTTGAA-CACTTGCCTTACCATCCACCGAGCTTGCAGTGTCTGGGAA 313
 QY 1429 ATGAAAGATCTGCGATGAGAACCTGCAAGAGCCCTGCAAAATTGACATGATGTCCT 1488
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 QY 1549 TCGGACATGCTGGGGATGACCTCCCAAAGCAGGCCCTGCTGTCCTCCCC 1608
 Db 192 TCGGACATGCTGGGGATGACCTCCCAAAGCAGGCCCTGCTGTCCTCCCC 133
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 Db 132 GCCTCCAGTCAATGGTACTACCCAGCC-TGGGTCTACCCCTCCATCCCTACAC 73
 QY 1668 TGTG-CGCAGAAGGGCGGCTCAGGTTGTCACCTCCACATGTCCTCTCCACA 1725
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KEYWORDS	EST; Homo sapiens (human)	Qy	515 TGGCAAATGGGCCCTTGTAGCATCTGTAACAAGTGGAGAGATGGCTGTGGCAAG 574
SOURCE	Homo sapiens	Db	526 TGGAAATGGGCCCTGTAGCATCTGTAACAAGTGGCTGTGGCAAG 585
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	Qy	575 CCAAGGCACCCCTGAGAGCTTCGGAGCAGAACAGATGGCCAGAATCTCA 634
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Db	586 CCAAGGCACCCCTGAGAGCTTCGGAGCAGAACAGATGGCCAGAATCTCA 645
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.	Qy	635 ACCGATTCCATACAGGACACATTGGAGGGACACCCGACTGGCCCAAATG 694
TITLE	Full-length cDNA libraries and normalization	Db	646 ACCGATTCCATACAGGACACATTCTGGAGGGACACCCGACTGGCCCAAATG 705
JOURNAL	On Feb 15, 2001 this sequence version replaced gi:12897130.	Qy	695 GAACCGTGAACAAACACTCTGGCATTTGACTTCAAAACAGTTAACCTTCCTGAGACTCA 764
COMMENT	Contact: Genoscope	Db	706 GAACTGTGAAATAACTCTGGCATTTGACTTCAAAACAGTTAACCTTCCTGAGACTCA 765
Genoscope - Centre National de Sequencage	BP 191 9106 EVRY cedex - France	Qy	755 ACAGAAATCACTCTGGAGAGCTTGGAAAGGGCATATGACATTGCGTGTGA 814
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr	Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f. For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DK008BH07QP1&cluster=6100.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DK008BH07QP1.	Db	766 ACAGAAATCACTCTGGAGGTATGGACTCAATGAGGTATGACATTGCGTGTGA 825
FEATURES	Location/Qualifiers	Qy	815 AGGTGTGAGGTTGAGACTGGGACTTGGAGCTTGGAAAGGGCATATGACATTGCGTGTGA 874
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	/db_xref="CS0DK008Y014"	Db	886 CCCGGCTCAGGATTCTCGCATCCAATGTCGCTCAAGTGGCTGTGCAGCTC 945
	/cell type="HELA CELLS COT 25-NORMALIZED"	Qy	935 CACCT-GCTCTCATCTACTCTCATCACACTCGATGCCGTATGGAT 982
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	/clone lib="Homo sapiens HEla CELLS COT 25-NORMALIZED"		
	/note="1st strand cdna was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cdna was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
BASE COUNT	244 a 265 c 282 g 199 t 4 others	RESULT 12	
ORIGIN		AL514330	1201 bp mRNA linear EST 08-MAY-2003
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		DEFINITION	CLOBB01ZH02 5'-PRIME, mRNA sequence.
		ACCESSION	AL514330
		VERSION	GI:30464215
		KEYWORDS	EST.
		SOURCE	Homo sapiens (human)
		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		REFERENCE	(bases 1 to 1201)
		AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
		TITLE	Full-length cDNA libraries and normalization
		JOURNAL	Unpublished
		COMMENT	On Feb 13, 2001 this sequence version replaced gi:12777824.
		CONTACT	Contact: Genoscope
			Genoscope - Centre National de Sequentage
			BP 191 9106 EVRY cedex - France
			Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
			Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f. For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CLOBB01ZH02&cluster=6100.f. Contact : Peng Liang Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CLOBB01ZH02&pi.
		FEATURES	Location/Qualifiers
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double-strand cDNA was digested with Not I and cloned into the Not I and EcoR sites of the pCMVSPORT 6 vector.

BASE COUNT 289 a 288 c 309 g 251 t 64 others

BASE COUNT	ORIGIN	Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps	3;					
289	a	108	CAGTCTCAGGCTCCCAAATCCAGGGACTCGGCCGCGGTATGGACAT	167	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003			
288	c	80	CGICCTCAGGCTCCCAATCCAGGGACTCGGCCGCGGTATGGACAT	167	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	1038	-MTGCCTTCYWWMAAAAACCCYTCCCCMA	1073	1201 bp	mRNA	linear	EST 05-MAY-2003			
309	g	168	TTCACTCAGTGCAGGAAACGGCAACGACTTGCCCTTCCTGCTGCTGACAT	167	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	166	ATTTCACTCAGTGCAGGAAACGGCAACGACTTGCCCTTCCTGCTGCTGACAT	225	1201 bp	mRNA	linear	EST 05-MAY-2003			
251	t	140	TTCACTCAGTGCAGGAAACGGCAACGACTTGCCCTTCCTGCTGCTGACAT	167	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	141	ATTTCACTCAGTGCAGGAAACGGCAACGACTTGCCCTTCCTGCTGCTGACAT	200	1201 bp	mRNA	linear	EST 05-MAY-2003			
64	others	228	GAACGACCTCACACAGGGAGCATCATGCTTCCTGACTGGCCCTGCCAGA	287	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	226	BXK63152	1201 bp	mRNA	linear	EST 05-MAY-2003	REFERENCE			
		200	GAACGACCTCACACAGGGAGCATCATGCTTCCTGACTGGCCCTGCCAGA	259	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	200	BX363152	1201 bp	mRNA	linear	EST 05-MAY-2003	AUTHORS			
		288	GGGGCGCTCTGCTGGTGTGAGATGTGTATGGGGGGACGGATCATGAA	347	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	260	BX363152.1	1201 bp	mRNA	linear	EST 05-MAY-2003	JOURNAL			
		260	GGGGCGCTCTGCTGGTGTGAGATGTGTATGGGGGGACGGATCATGAA	319	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	260	BX363152.1	1201 bp	mRNA	linear	EST 05-MAY-2003	KEYWORDS			
		348	CGCTGGGATGACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	407	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	320	CGCTGGGATGACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	379	1201 bp	mRNA	linear	EST 05-MAY-2003	SOURCE		
		408	GAACATGCGCTTITGGGCCAAGATCGTGTGCTGCTGCTGCTGCTGCTG	467	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	408	BXK63152.1	1201 bp	mRNA	linear	EST 05-MAY-2003	ORGANISM			
		380	GAAGCTTATGGATGACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG	439	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	380	BXK63152.1	1201 bp	mRNA	linear	EST 05-MAY-2003	CONTACT			
		468	GCACATAGCGCTTITGGGCCAAGATCGTGTGCTGCTGCTGCTGCTG	527	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	468	BXK63152.1	1201 bp	mRNA	linear	EST 05-MAY-2003	GENOSCOPE			
		440	GCACATAGCGCTTITGGGCCAAGATCGTGTGCTGCTGCTGCTGCTG	499	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	440	BXK63152.1	1201 bp	mRNA	linear	EST 05-MAY-2003	GENOSCOPE - Centre National de Sequencing			
		528	CCTCTCAGCATCTAACAGTATGGAGAGATGCTGCTGCTGCTGCTG	587	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	528	BP 191 9106 EVRY Cedex - France	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY			
		560	GAGAGCTTCTCCAGAGAGATGGCAAGATCTCAACAGGACATGCTGCTG	619	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	560	I (bases 1 to 1201)	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY			
		500	CCTGTCAGCCTCTGTACAGTATGGAGAGATGGCAACGCTGCTGCTG	559	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	500	I (bases 1 to 1201)	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY			
		588	GGAGAGCTTCTCCAGAGAGATGGCAAGATCTCAACAGCTTCCATA	647	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	588	I (bases 1 to 1201)	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY			
		560	GAGAGCTTCTCCAGAGAGATGGCAACGCTGCTGCTGCTGCTGCTG	619	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	560	I (bases 1 to 1201)	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY			
		648	CAAGGACACATCTCGAGAGGGGACACCCACTGGCCCGAAATGGACAC	707	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	QY	648	I (bases 1 to 1201)	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY			
		620	MAAGGAMATTCCTGAAGGGGACACCCGACTGGCCCGAAATGGACAC	679	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.7%; Pred. No. 1.3e-128; Mismatches 21; Indels 3; Gaps 3;	Db	620	I (bases 1 to 1201)	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY			
		708	ACACTCTGCTATGGTCAACAGCTTAATCTGCTGCTGCTGCTGCTG	767	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	QY	708	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
		680	AMACTCTGCTATGGTCAACAGCTTAATCTGCTGCTGCTGCTGCTG	739	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	Db	680	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
		768	TGGAGACTTATGGAGGGCCCTGCAGGCCAACATGCTGCTGCTGCTG	827	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	QY	768	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
		740	TGGAGACTTATGGAGGGCCCTGCAGGCCAACATGCTGCTGCTGCTG	799	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	Db	740	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
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		888	TTCTCGCATCAATGTCGCTGCTGCTGCTGCTGCTGCTGCTG	947	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	QY	888	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
		860	TTCTCGCATCAATGTCGCTGCTGCTGCTGCTGCTGCTGCTG	919	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	Db	860	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
		948	TCCTACTCTCATCACACACTGATGGTCTGCTGCTGCTGCTG	1007	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	QY	948	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
		920	TCCTACTCTCATCACACACTGATGGTCTGCTGCTGCTGCTG	979	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	Db	920	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
		1008	CACCAATTGGTGGGACGAGCCAGGGCTGAGTTGCTGAGATGAT	1067	51.1%	Score 915; DB 9; Length 1201; Best Local Similarity 94.5%; Pred. No. 3e-128; Mismatches 37; Indels 7; Gaps 5;	QY	1008	QY	1068	CATGCCCTCTCACACACTAGACCCCTCATCCA	1104	1201 bp	mRNA	linear	EST 05-MAY-2003	LIBRARY
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	Qy	346 AACCGTGGGATGACACCCCTGCATTCGGACGGTCACTGGAGACCGTGATATTGTA 405		
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	Qy	406 CAGAAGCTATTGCACTAACAGGAGACATCAATGCACTGGAAATGTGCC 465		
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	Qy	466 CTGCACTATGCGTTTGGGCCAAGATCACTGGCAGGACCTGTGCAATGG 525		
	Db	441 CTGCACTATGCGTTTGGGCCAAGATCACTGGCAGGACCTGTGCAATGG 500		
	Qy	526 GCCCTTGACGATCTAACAGTATGAGGATGCTGTGACAAGGCCAAGGACCC 585		
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	Qy	586 CTGAGAGAGCTCTCCGAGCCAGAGAAGATGGCCAATCTAACCGTATTCA 645		
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	Qy	766 TCTGGAGGACTATGGAAAGGGCCAAATGACATGTCGTCGAGGCTGTCGAG 825		
	Db	741 TCTGGAGGACTATGGAAAGGGCCAAATGACATGTCGTCGAGGCTGTCGAG 800		
	Qy	826 GTTCGAGACTGCAAGGAGAGGAACTGCAATGGAAAGGCTCCCGGMONGG 885		
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	Qy	886 ATTTTCTGCACTCAAACTGCTCCACCTGTCTGCACTGTCT 945		
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	Qy	946 CATCCCTACTCTCATCACACTGGATCCGTATGGCCCTACATGAA 1005		
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	Qy	1006 GGCACTAAATTGCTGCACTGGATCCGTATGGCCCTACATGAAAGG 1065		
	Db	977 GGACCAATTCTCTCATCACACKGATGCGTGGATGGCTCYCT--TAARTFTCTYTGATGAMWKGAAGG 1033		
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DEFINITION		BX340064 Homo sapiens PLACENTA COT 25- NORMALIZED Homo sapiens cDNA clone CSOD1081YL01		
ACCESSION	BX340064	3-PRIME, mRNA sequence.		
VERSION	BX340064.1	GI:30333861		
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SOURCE	ORGANISM	Homo sapiens		
	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;			
REFERENCE	1 (bases 1 to 1201)			
AUTHORS	Liu,W., Gruber,C., Jesse, J. and Polayes,D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
COMMENT	Contact: Genoscope Genoscope - Centre National de Séquencage BP 191 91006 EVRY cedex - France			

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f. For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOD1081CF01NP1&cluster=6100.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope Sequence ID : CSOD1081CF01NP1.				
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		/note="First strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library was normalized."		
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		Db	897 AACAAAGAAAGCAGGAGGACTCAATGAAGAGTGTCCCCTGTCGAGATTCTCGATCC 838	
		Qy	900 AAATGIGCTCCAGTGTAGGTGCTCCACCTGCTCTCATCTACTCTCATCT 959	
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		Qy	1020 CGTGGACGAGGCAAGGCCGCTGCAAGTTGCTGAGCTGGCTGGCATGGCCATGGCTCTCT 1079	
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		Qy	1080 ACACACATAGCTGACTGCCGAATTAGCATGGCTGATGTCAGTCATGCCAACTGCTGAGTGTGA 1139	
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		Qy	1200 TCGCATGTTATGCACTCGCCGCTGGTAACCTGGCAAGCTCTGGAGAAAGCTGAGACAC 1259	
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ACCESSION BX340065 CSOD1081YL01 5'-PRIME, mRNA sequence.
VERSION BX340065.1 GI:30335869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 1201) Homo.
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequençage
 BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6100.f. For more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOD1081CF01P&cluster=6100.f>. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Parady Avenue Genoscope sequence ID : CSOD1081CF01P1.
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BASE COUNT 288 a 295 c 315 g 252 t 51 others
ORIGIN
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